## **WEST Search History**

DATE: Friday, April 12, 2002

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT	; PLUR=YES; OP=AND		
L17	L16 and arthur.in.	14	L17
L16	sands.in.	417	L16
L15	zambrowicz.in.	6	L15
L14	abuin.in.	1	L14
L13	L12 and glenn.in.	6	L13
L12	friedrich.in.	6503	L12
L11	wattler.in.	1	L11
L10	L9 and john.in.	22	L10
L9	scoville.in.	48	L9
L8	15 and 17	0	L8
L7	gregory.in.	14821	L7
L6	L5 and gregory.in.	0	L6
L5	donoho.in.	97	L5
L4	hilbun.in.	1	L4
L3	L2 and 11	11	L3
L2	alexander.in.	11250	L2
L1	turner.in.	2993	L1

END OF SEARCH HISTORY

Sequence Sequence Sequence

Sequence 25, Appl Sequence 25, Appl Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 49, Appli Sequence 16, Appli Sequence 16, Appli Sequence 5, Appli Sequence 6, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli

ALIGNMENTS

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Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
US-08-949-386-24
US-08-450-562-24
US-08-949-386-25
5200327-1
US-08-318-193-1
5200327-3
US-08-318-193-7
5200327-3
US-08-318-193-7
5200327-3
US-08-318-193-9
US-08-442-063A-49
US-08-442-063A-48
US-09-475-316A-16
US-09-475-316A-16
US-08-676-974-5
US-08-676-974-5
                                                                                                                                                                             US-08-717-294-42
US-09-385-028-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY-AGENT INFORMATION:
NAME: BENT, Stephen A.
REGIGTRATION NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEFAX: (703)683-4109
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STRANDEDNESS: single
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Patent No. 539
Sequence 2, A
Sequence 4, A
Sequence 24,
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Sequence 26,
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Sequence 3,
Sequence 4,
                                                                           April 11, 2002, 13:42:33 ; Search time 127.46 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
            4.5
Compugen Ltd.
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US-08-111-939-1

US-08-104-196-1

US-08-140-1

US-08-123-463-14

US-09-324-867-1

US-09-324-867-1

US-09-324-867-1

US-09-324-10080-7

US-09-393-3

US-09-393-3

US-09-192-115-15

US-09-192-115-15

US-09-192-115-15

US-09-192-115-15

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US-09-192-115-17

US-09-193-115-17

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US-08-149-097D-24
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Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0
            GenCore
Copyright (c) 1993
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Maximum DB seq length: 200000000
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3924
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Match Length DB
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Perfect score:
Sequence:
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1365 CAGTGGATCGAGGTGGACACCCGAAGGACAACTCGGTTCACGGGCGTCATCACTCAGGGC 1424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1605 ATCTATCACTCACCTGGAACGGTAGCCTGTGCATGCGCCTGGAGGTGCTAGGCTGC 1661
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1%; Score 41.4; DB 1; Length 3 48.8%; Pred. No. 0.098; tive 0; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/804,196
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5874256el Patent Department
                                                 02481.1321-00000
                                                                                                                                                                                                                                                                                                      STRAIN: osteoblastic cell line MC3T3E1
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Patent No. 5874256
GENERAL INFORMATION:
APPLICANT: Bertina, Rogier
APPLICANT: Reitsma, Pieter
TITLE OF INVENTION: A method for d
TITLE OF INVENTION: trisk for throm
TITLE OF INVENTION: thrombosis and
NIMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                          33,694
                                      REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                      TELEFAX: 202-408-4000 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA to MRNA ORIGINAL SOURCE: ORGANISM: Mus musculus
                                                                                                                                                           LENGTH: 3728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
      NAME: Forman, David S. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 145; Conservative
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY:
; LOCATION:
US-08-111-939-1
                                                                                                                                                                                                                          TOPOLOGY:
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US-08-804-196-1
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      Length 7218;
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Patent No. 560951
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rawai, Shinji
APPLICANT: Okazaki, Makoto
APPLICANT: Anann, Egon
TITLE OF INVENTION: Bone-Related Carboxypeptidase-Like
TITLE OF INVENTION: Protein and Process for its Production
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
Query Match 1.2%; Score 45.2; DB 1; Length 7 Best Local Similarity 6.1%; Pred. No. 0.011; Matches 26; Conservative 216; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING-SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/111,939
FILING DATE: 26-A0G-1993
FILING DATE: 26-A0G-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
STREET: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 324033/92
FILING DATE: 03-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 230029/92
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
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Length 3728;

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6621 TTTTGAAGGAAATACTAATACCAAAGGACATGTGAAGAACTTTTTCAACCCCCCAATCAT 6680
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Patent No. 6066778
GENERAL INFORMATION:
APPLICANT: Ginsburg, David
APPLICANT: Cui, Jisong
TITLE OF INVENTION: Compositions And Methods For Screenin
TITLE OF INVENTION: Compounds For Anticoagulant Activity
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-LOOS/MS-DOS
SOFWARE: Patentin Rclease #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 154;
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                       FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/454,353
FILING DATE: 06-UNN-1995
ATTORNEY/AGENT INFORMATION:
    US/08/658,340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America 2IP: 94104
                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 948-7400
TELEPRAX: (301) 948-9751
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: (509 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                34,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 49.8
Matches 165; Conservative
                                                                                                                                        NAME: Gormley, Mary E. REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-746-111-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40.6; DB 2; Length 6909;
Pred. No. 0.24;
0; Mismatches 154; Indels 12;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6741 ACTCTTTGGCTGTGATATTTACTAGAATTGA 6771
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              PALLON NUMBER: US 08/454,353
PILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: GORMLEY, MARY E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 948-7400
TELEPHONE: (301) 948-751
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6999 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-58-340-1
Sequence 1, Application US/08658340
Fatcht No. 5910576
Patent No. 5910576
GENERAL INFORMATION:
APPLICANT: Bertina, Rogier
APPLICANT: Bertina, Pieter
TITLE OF INVENTION: Tisk for throm
WHABER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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Best Local Similarity 49.8'
Matches 165; Conservative
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 06-JUN-:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                            TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: CDNA
US-08-804-196-1
                                                                                                                                                                                                                                                                                                                           unknown
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STATE: Maryland
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FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                              Length 6909;
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                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATE: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                    0.24;
                                                                                                                                                                                                                                                                                                                                                                Score 40.6;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6741 ACTCTTTGGCTGTGATATTTACTAGAATTGA 6771
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APPLICATION NUMBER: US/08/746,111
FILING DATE: 06-NOV-1996
CLASSIFICATION:
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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
                                              ATTORNEY AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-838
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 6909 base pairs
                                                                                                                                                                                                                                                                                                                                                                1.0%;
                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 49.8 Matches 165; Conservative
                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
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APPLICANT: Cameron, Cherie
APPLICANT: Cameron, Cherie
APPLICANT: No. 62516321ey, Colleen
APPLICANT: Hough, Christine
APPLICANT: Hough, Christine
TITLE OF INVENTION: Canine Factor VIII Gene, Protein and Methods of Use
FILE REFERENCE: 1669.0010002/JAG/BJD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 agagattacagcagtggccacgcagggaagatacggaagctctgactgggtgacgagtta 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207; Mismatches 178;
                                                                                                                                                      REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/324,867A CURRENT FILING DATE: 1999-06-03
                                       FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.08;
                                                                                                                                                                                                                         (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                    LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.2%;
                                                                                                                                   NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                   TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Lillicrap, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                   , CLUNE: PTZGPt-Fls
US-08-232-463-14
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Matches 21; Conserv
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3722 teggaggggtgatagcagtggtgatatteateatettetgtateategeeateatgaeee 3781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        459 TGGTCGGCATCATCGCCGGCCCCGTCTTCCTTATCATTATCATCATCATCTTC 518
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ADDRESSEE: Genetics Institute Inc.- Legal Affairs
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.0%; Score 37.8; DB Best Local Similarity 57.0%; Pred. No. 0.68; Matches 69; Conservative 0; Mismatches
APPLICATION NUMBER: US/08/123,934A
FILING DATE: 17-SEP-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876 1170
TELEPHONE: 617 876 1170
TELEPHONE: 617 876 1170
TELEPHONE: 617 876 1170
SEQUENCE CHARACTERISTICS:
LENGTH: 1647 base pairs
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GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,934
FILING DATE: 17-SEP-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
RESISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OFFICIONS OFFICE OFFICE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02140
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LOCATION:
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PCT-US94-10080-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6696 teaggeammtmaccemmagagtggetgemagtggaetteeggaagaeeatgaaagteae 6755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6936 ggtggctcgctacgtgcgcctgcacccgcagagctgggcgcaccacatcgcctgaggct 6995
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ADDRESSEE: Genetics Institute Inc.- Legal Affairs STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred. No. 1.2;
EARLIER APPLICATION NUMBER: 09/035,141
EARLIER FILING DATE: 1998-03-059
EARLIER PRILIGATION NUMBER: 60/039,953
EARLIER FILING DATE: 1997-03-06
NUMBER OF SEQ ID NOS: 63
SEQ ID NO 1
LENGTH: 7032
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APPLICANT: WOZNEY, John
APPLICANT: CELESTE, Anthony J.
APPLICANT: THIES, R. SCOLT
APPLICANT: TAMANI, NO. 62912066ru
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08123934A
Patent No. 6291206
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                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Canis familiaris FEATURE:
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Matches 173; Conservative
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MEDIUM TYPE: Floppy
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) LOCATION: 1..7029
US-09-324-867-1
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US-08-123-934A-7
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APPLICANT: Miyazono, Kohei, Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3722 tcggaggggtgatagcagtggtgatattcatcatcttctgtatcatcggcatcatgaccc 3781
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MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: THE PC-DOS
                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: LUD 5298.1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.0%; Score 37.8; DE Best Local Similarity 57.0%; Pred. No. 0.8; Matches 69; Conservative 0; Mismatches
                                               FILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: July 2, 1993
APPLICATION NUMBER: 931609.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: OCTOBER 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-598
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2160 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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CLEET: 805 Third Avenue
CITY: New York City
ZIP: 10022
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MOLECULE TYPE: cDNA
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CORRESPONDENCE ADDRESS:
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Patent No. 6207814
GENERAL INFORMATION:
APPLICANT: MIXAZONO, Kohei
TEN DIJKE, Petra
FRANZEN, Petra
FRANZEN, Petra
YAMASHTA, Hidetoshi
HELDIN, Carl-Henrik
TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
AND THEIR USE
AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 1647;
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COUNTRY: USA
ZIP: 10103
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: NO. 6207814ember. 17, 1993
APPLICATION NUMBER: GB 9224057.1
FILING DATE: NO. 6207814ember 17, 1992
APPLICATION NUMBER: GB 9304677.9
FILING DATE: March 8, 1993
APPLICATION NUMBER: GB 9304680.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37.8; DB
Pred. No. 0.68;
0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-8850
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1647 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: W-101
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.0%;
Matches 69; Conservative
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80..1594
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; LOCATION;
PCT-US94-10080-7
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DB 4; Length 2160;

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                                                                                 GENERAL INFORMATION:
APPLICANT: Barber, Robert
APPLICANT: Barber, Robert
APPLICANT: Witthun, Vernon
TITLE OF INVENTION: Remediation
FILE REFERENCE: 960296.95505
CURRENT APPLICATION NUMBER: US/09/192,983A
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/919,953
EARLIER APPLICATION NUMBER: 08/919,953
EARLIER PILING DATE: 1996-02-28
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 4826
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APPLICANT: Itoh, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8776
CURRENT APPLICATION NUMBER: US/09/214,278
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 3955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.0%; Score 37.8; DB 4; Length 48. Best Local Similarity 48.8%; Pred. No. 1.3; Matches 102; Conservative 0; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2162 gtgagtgtggcctagacgagagctgcctg 2190
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                           Sequence 3, Application US/09192983A Patent No. 6242244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09214278 Patent No. 6291210 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Rhodobacter sphaeroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: CDS
LOCATION: (215)..(895)
FEATURE:
NAME/KEY: CDS
LOCATION: (993)..(2165)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (2236)..(4437)
US-09-192-983-3
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-214-278-4
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                                                                           FLILING DATE:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-october-1995
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-NO. 6271365ember-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 930467.9
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 931047.6
FILING DATE: 8-March-1993
PRIOR APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION NUMBER: 9313763.6
FILING DATE: 3-August-1993
PRIOR APPLICATION NUMBER: 931344.5
FILING DATE: 15-October-1993
APPLICATION NUMBER: 913609.2
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlel, Vincet
RECISTATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELEPHONE: C121) 8838-3884
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
CONTINUE FRIESTICS:
CONTINUE FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
CONTINUE FRIESTICS:
CONTINUE 
                              APPLICATION NUMBER: US/09/395,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2160 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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; LOCATION:
US-09-395-115-15
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Length 4315;

DB 3;

Score 37.4; D Pred. No. 1.6; 0; Mismatches

1.0%;

56; Indels

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Conservative
  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08882046
Patent No. 6136952
GENERAL INFORMATION:
APPLICANT: Li, Linheng
APPLICANT: Krantz, Ian D.
APPLICANT: Krantz, Ian D.
TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
TITLE OF INVENTION: Nucleic Acids and Methods of Use
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/882,046
FILING DATE: 25-JUN-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNDBER: 31,815
REFERENCE/DOCKET NUMBER: P-UW
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-9001
SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                 | NAME/KEY: $19_peptide
| LOCATION: (12)..(89)
| NAME/KEY: mat_peptide
| LOCATION: (90)..(3725)
| US-09-214-278-4
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16..3460
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US-08-882-046-3
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                     LOCATION:
NAME/KEY:
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1638 catcaaagacaggtgtttgccaaactactgtgaacatggaggaagctgctcccagtcctg 1697
                                                                                                        1698 gactaccttctattgtaactgcagtgacacaagttacactggtgccacctgccacaactc 1757
                                                                                                                                            2058 GCCCTCCTTCTCTGCCGGGACGCTGGAGGGTCGTACTTGCACAATAC 2117
                                                    1998 CAAGAACAGCAGCTGCCTGCCCAACCCCTGTGTGAATGGTGGCACCTGCGTGGGCAGCGG 2057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
TITLE OF INVENTION: NUCLECTIDE AND PROTEIN SEQUENCES OF THE
TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
UNDBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READSHLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,159
FILING DATE: 07-MAR-1995
CLASSIFICATION: 435
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55.9%; Pred. No. 1.6;
tve 0; Mismatches 56;
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Fleming, Robert J.
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ish-Horowicz, David
Henrique, Domingos M.P.
Lewis, Julian H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALUCHARATOR MAISTOCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: (614) PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08400159 Patent No. 5869282 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.0%;
Best Local Similarity 55.9%;
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
EDNESS: double
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036-2711
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2071 CAAGAACAGCAGCTGCCTGCCCAACCCCTGTGTGAATGGTGGCACCTGCGTGGGCAGCGG 2130
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<sup>2131</sup> GGCTTCTTCTCTGCTGCTTGCTGGGTGGGTGGTTGTTGCTTGCACTTGATAC 2190 qq

<sup>1758</sup> catctac 1764 || || || 2191 CAACGAC 2197 oy op

Search completed: April 11, 2002, 14:48:56 Job time: 3983 sec

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Sequence 2, Sequence 2,

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Sequence 6, Appendix No. 19 Per 19 Pe

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US-08-162-402B-3
US-07-607-538C-2
US-08-162-402B-6
US-08-162-402B-8
US-08-111-939-19
US-08-111-939-19
US-08-111-939-13
US-08-111-939-25
US-09-191-647-7
US-09-191-647-7
US-09-540-153-7
PCT-US91-09055-2
                                                                                                                                                                                              US-08-670-707A-39
US-09-037-601-39
                                                                                                                                                                                    -09-324-867-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: Fast SEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/644,271
FILING DATE: 10-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/008,657
FILING DATE: 15-DEC-1995
ATTORNEY,AGENT INFORMATION:
NAME: CODERT, ROBERT J
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 195A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1940 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 217
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11480
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TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: Rat Agrin
; LOCATION: 1...1940
; OTHER INFORMATION:
US-08-644-271-30
 US-08-644-271-30
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Sequence 2, Appli
Sequence 4, Appli
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Sequence 24, Appli
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Sequence 32, Appli
Sequence 183, Appli
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Sequence 12, Appli
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Sequence 12, Appli
Sequence 12, Appli
Sequence 14, Appli
Sequence 16, Appli
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129.665 Million cell updates/sec
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Patent No. 5444158
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                 US-09-770-643A-2
6962
1 MDSLPRLTSVLTLLFSGLWH.....FRNEIDLQNTVSECKREYFI 1307
                                                                                  April 11, 2002, 13:43:08; Search time 226.83 Seconds
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2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/pcarus_comB.pep:*
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-111-939-2
US-08-746-111-5
US-08-162-402B-9
US-08-936-135-8
                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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US-08-162-402B-12
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US-09-540-153-2
US-08-644-271-32
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                                                                                                                                                                                                                        212252 seqs, 22503292 residues
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Maximum Match 100%
Listing first 45 summaries
                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Query
Match Length DB
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Sequence:
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                                                                        1244 FTCSCTAGRGGSVCEKVQPPSMP---AFKGHSFLAFPTLRAYHTLRLALEFRALETEGLL 1300
                                                                                                                ------QTV-----DETAGSRPFLADFNGFS-YLELKGLH- 1543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      967 ICHNGGKCVEKHNGYLCDCTNSPYEGPFCKKEV-----SAVFEAGTSVTYMFQEPY 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1018 PVTKNISLSSSAIYTDSAPSKENIALSFVTTQAPSLLLFINSSSQ--DFVVVLLCKNGSL 1075
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                                                  ---EPQIVPITEVNSSGSYLLLPGTPQIDGLSVSFQFRTWNKDGLL 405
                                                                                                 LSTELSEGSGTLLLSLEGGILRLVIQKMTERVAEILTG-SNLNDGLWHSVSINARRNRIT 464
                                                                                                                                                  LTLDDEA-----APPAPDSTWVQIYSGNSYYFGGCPDN----LTDSQCLNPIKAFQGCMR 515
                           Gaps
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                                                                                                                                                                                                                                                    FYCNCSDTSYTGATCHNSIYEQSCEVYRHQGNTAGFFYIDSDGSGPLGPLQVYCNITEDK
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                         Indels 269;
 Length 1940;
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;Patent No. 5444158

; APPLICANT: ENVIOLE. EVA;SANES, JOSHUA

; TILLE OF INVENTION: MEROSIN, NUCLEIC ACIDS ENCODING,

;FRAGMENTS AND USES THEREOF

; NUMBER OF SEQUENCES: 4

; CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1881 DTDGALWLGGL-QKLPVGQALPKAYGTGFVGCLRDVVVGH 1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVIRSLTLGKVTENLGLDSEVAKANAMGFAGCMSSVQYNH 1173
           Similarity 21.6%; Pred. No. 2.9e-23;
30; Conservative 115; Mismatches 306;
 DB 2;
5.2%; Score 360.5; DB 2
21.6%; Pred. No. 2.9e-23;
                         Matches 190;
 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----SSPDYVGVTKECSLE----NVY----TVSF---PKPGFVELSPVPIDVG-TE 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKIWTSVQHNNTELTRVRGANPEKP-----YAMALDYG-----GSMEQLEA 667
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                                                                                                                                                                                                                                                                  Length 1130;
                                                                                                                                                                                                                                                                      DB 6;
                                                                                                                                                                                                                                                                                                             389;
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20.0%; Pred. No. 4.3e-20;
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APPLICATION NUMBER: US/08/87
FILING DATE: 08-UU-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 587,689
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 472,319
FILING DATE: 30-JAN-1990
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5444158-2
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Best Local Si
Matches 221;
                                                                                                                                                         ;SEQ ID NO:2
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SLSSSAIYTDSAPSKENIALSFVTTQAPSLLLFINSSSQDFV--
 DB 2;
                              224; Conservative 150; Mismatches 378;
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   4.6%; Score 320.5;
                Pred. No. 5
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                                          961 CSSYGSICHNGGKCVEKHNGYLCDCTNSPYEGPFCKKEVSAV--FEAGTSVTYMFQEPYP 1018
                                                                                                   1019 VTKNISLSSSAIYTDSAPSKENIALSFVTTQAPSLLLFINSSSQDFVVVLLCKNGSLQVR 1078
                                                                                                                                                                            || :|  |  |  |  || || 1038 GHLCDGQWHKVT-----ANKIKHRIELTVDGNQVEAQSPNPASTSADTNDPVFVGGFPD 1091
                                                                      -SSF----HVGTCFANAQRGTYFDGTG-----FAK----AVGGFKVGLDLLVEFERTT
                                                                                                                                 TTTGVLLGI-----SSQKMDGMGIEMIDEK---LMFHVDNGAGRFTAVY-----DAGVP
                                                                                                                                                            YHLNKEETHVFTIDADNFANRRMHHLKINREGRELTIQMDQQLRLS------
                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08460309
Patent No. 5837496
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Fregments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/460,309
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-3NN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
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                                                                                                                                                                                                                   ----YNFSPEVEFR-VIRSLTLGKVT 1145
                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1130 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE:
US-08-460-309-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ropology:
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                                                                                                                                                                                                                                                                                                       -08-460-309-2
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49; -------FATTTTGVLLGISSOKMDGMGIEMIDEKLMFHVDNGAG 1026 -----LQVRYHLNKEETHVFTIDADNFANRRMHHLKINREGRELTIQMDQQLRLS--- 1124 SICHNGGKCVEKHNGYLCDCTNSPYEGPFCKKEVSAV--FEAGTSVTYMFQEPYPVTKNI 1023 699 |: :| |: || | || QVED-----SEGTIQFDGEGYALVSRPIRWYPNISTVMFKFRTFSSSALLMYL 400 799 -DDTKVKNRLTIELE-----VRTEAESGLLFYMAAINHADFATVQLRNGLPY-FSYD 848 915 LFVGGT----SSRQKGFL----GCIRSLHLNGQKMDLEERAKVTSGVRPGCPGHCSSYG 965 205 ISLKFKSMQGDGVLFH-GEGQRGDHITLELQKGRLALHLNLGDSKARLSSSLPSATLGSL 263 LDDQHWHXVLIERVGKQVNFTVD------KHTQHFRTKGETDALDIDYE--LSFGG 311 KDHLPVIQIVI------TDTD-----RSNSEAAWRIGPLRCYGDRRFWNAVSF 796 797 YTEASYLHFPTFHAEFSADISFFFKTTALSGV--FLENLGIKDFIRLEISSPSEITFAID 854 VGNGPVELVVQSPSLLNDNQWHYVRAERNLKETSLQVDNLPRSTRETSEEGHFRLQLNSQ 914 IPVPGKPGTFLKK-----NFHGCIENLYYNGVNIIXLAKRRKHQIYTVGNVTFSCSEP 364 ----LSTELSEGSGTLLLSLEGGILRLVIQKMTERVAEILTGSNLNDGLWHSVSIN 457 -----DIQHFCNCDADKDEWTNDTGFLSF 754 :|| :|: :: | |: :| IDDSYWYRIVASRTGRNGTISVRALDGPKASIVPSTHHSTSPPGYTILDVDANAMLFVGG ----LSVSFQFRTWNKDGLL---401 ATRDLRDFMSVELTDGHIKVSYDLGSG------MASVVSNONHNDGKWKSFTLS LKKYSGCLKDIEISRTPYNILSSPDYVGVTKG------CSLENVYTVSFPKPG-SCSQSWTTFYCNCSDTSYTGATCHNSIYEQSCEVYRHQGNTAGFFYIDSDGSGPLGPLQV 621 YCNITEDKIWISVQHNNTELTRVRGANPEKPYAMALDYG-----GSMEQLEAVI---------RRKRRQTGQAYYVILLNRGRLEVHLSTGARTMRKIVIRPE ----DGSEHCEQEVAYHCRRSRLLNTPDGTPFTWWIGRSNERHP-----YWGGSPPGV 635 PNLFHDGREH----SVHVERTRGIFTVQVDENRRYMQNLTVEQPIEVKKLFVGGAPPEF ARRNRITLTL-----DDEAAPPAPDSTWVQIYSGNSYYFGGCPDNLTDSQCLNP---IKAFQGCMRLIFIDNQP-----KDLISVQQGSLGNFSDLHIDLCSIKDRCLPNYCEHGG QPSPLRNIPPFEGCIWNLVINSVPMDFARPVSFKNADIGRCAHQKLREDE------950 ---HVGTCFANAQRGTYFDGTG-----FAK----AVGGFKVGLDLLVEFE-----Length 1130; 1075

SADT 1080 Db	da -	O	Db 401	Qy 458	Oy 507 IKARQGCMRLIFIDNQPKDLISVQGG	Qy 561 SCSQSWTTFYCNCSDTSYTGATCHNSIYEQSCEVYRHQGNTAGFFYIDSDGSGPLGPLQV	Qy 621 YCNITEDKIWTSVQHNNTELTRVRGANPEKPYAMALDYG-	ОУ 670БGSEH 	QY 719 QQCECGLDESCL	Qy 755 KDHLPVTQIVITDTDRSNSEAAWRIGPLRCYGDRRFWNAVSF	Qy 797 YTEASYLHFPTFHAEFSADISFFFKTTALSGVFLENLGIKDFIRLEISSPSEITFAID  1	Qy 855 VGNGPVELVVQSPSLLANDNOWHYVRAERNLKETSLQVDNLPRSTRETSEGHFRLQLNSQ 	Qy 915 LFVGGTSCRQKGFLGCIRSLHLNGQKMDLEERA	Qy 966 SICHNGGKCVEKHNGYLCDCTNSPYEGPFCKKEVSAVFEAGTSYTYMFQEPYPVTKNI	QY 1024 SLSSSALYTDSAPSKENIALSFVJTQAPSLLLFINSSGOPFV       :    :  :		SL 263  Db 1081 NDPVFVGGFPDDLKQFGLTSIPFRGCIRSLKLTKGT 243
Db 1027 RFTAVYDAGVPGHLCDGQWHKVTANKIKHRIELTVDGNQVEAQSPNPASTSAL	QY 1125YNFSPEVEFR-VIRSLTLGKVT 1145 DD 1081 NDPVFVGGFPDDLKQFGLTTSIPFRGCIRSLKLTKGT 1117		RESULT 4 US-08-125-077-2 Sequence 2, Application US/08125077	Fatent No. 5872231 Patent No. 5872231 5840863 GENERAL INFORMATION:	APPLICANT: Engvall, Eva APPLICANT: Leivo, Ilmo TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin TITLE OF INVENTION: Fragments and Uses Thereof	OF SEQUENCES: ONDENCE ADDRESS SSEE: Campbell T: 4370 La Jol	CITY: San Diego STATE: California COUNTRY: USA ZIP: 92122	ADABLE FORM: PE: Floppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DOS	CURRENT APPLICATION UNMBER: US/08/125,077  PILING DATE: 22-SEP-1993	PRIOR APPLICATION DATA: APPLICATION NUMBER: US PCT/US 94/10730 FILING DATE: 21-SEP-1994	A: US N-199 A:	AFFLICATION NOMBER: 27-701-1992 ATTORNEY/AGENT INFORMATION: NAME: Campbell, Cathryn A. PRGISTREATION NIMBER: 31 815	REFERENCE/DOCKET NUMBER: P-LA 9721 TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001 TELEPAX: (619) 535-8049	INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1.130 amino acids TYPE: amino acids	ZE COC	 ISLKFKSMQCDGVLFH-GEGQRGDHITLELQKGRLALHLNLGDSKARLSSSLPSATLGS	Db 190 IVVNVKTAVADNLLFYLGSAKFIDFLAIEMRKGKVSFLWDVGSGVGRVEYPDLT

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2430 RIQKQANISIVDIDINQEENIATSSSGNNFGLDLKADDKIYFGGLPTLRNLSMKARPEVN 2489
                                                                                                                                                                                                                                                                -------RRKRRQTGQAYYVILLNRGRLEVHLSTGARTMRKIVIRPE 2615
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                                                                                                                                                                                                                                                                                                           ----DGSEHCEQEVAYHCRRSRLLNTPDGTPFTWWIGRSNERHP-----YWGGSPPGV 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFVGGT----SSRQKGFL----GCIRSLHLNGQKMDLEERAKVTSGVRPGCPGHCSSYG 965
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                                             IKAFQCCMRLIFIDNQP ----KDLISVQQGSLGNFSDLHIDLCSIKDRCLPNYCEHGG
                                                                                                                                 SCSQSWTTFYCNCSDTSYTGATCHNSIYEQSCEVYRHQGNTAGFFYIDSDGSGPLGPLQV
                                                                                                                                                                                                                       YCNITEDKIWTSVQHNNTELTRVRGANPEKPYAMALDYG------GSMEQLEAVI---
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Patent No. 5872231

Patent No. 5872231 5840863

GENERAL INFORMATION:

APPLICANT: Engvall, Eva

APPLICANT: Leivo, Ilmo

TITLE OF INVENTION: Pragments and Uses Thereof

NUMBER OF SEQUENCE: 23

CORRESPONDENCE ADDRESS:

ADDRESSE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
STRIE: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3062 NDPVFVGGFPDDLKQFGLTTSIPFRGCIRSLKLTKGT 3098
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                                                                                      LKKYSGCLKDIEISRTPYNILSSPDYVGVTKG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 LDDQHWHXVLIERVGKQVNFTVD------KHTQHFRTKGETDALDIDYE--LSFGG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          458 ARRNRITLIL ------DDEAAPPAPDSTWVQIYSGNSYYFGGCPDNLTDSQCLNP--- 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 ISLKFKSMQGDGVLFH-GEGQRGDHITLELQKGRLALHLNLGDSKARLSSSLPSATLGSL 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365 QIVPITFVNSSGSYLLLPGTPQIDG------LSVSFQFRTWNKDGLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    •••----LSTELSEGSGTLLLSLEGGILRLVIQKMTERVAEILTGSNLNDGLWHSVSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3111;
               APPLICANT: Leivo, ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                      JUNESSE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
STATE: San Diego
STATE: California
                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 4.6%; Score 320.5; DB 2; Best Local Similarity 20.1%; Pred. No. 3.3e-19; Matches 224; Conservative 150; Mismatches 378;
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR PELICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION NUMBER: US 07/472,319
FILING DATE: 27-UL-1992
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-UL-1992
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-UL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
TELEPAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3111 amino acids
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Engvall, Eva
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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2721 -DGAAPAEIVIQPEPVPTPAFPTPTPVLTHGPCAAESEPALLIGSKQFGLSRNSHIAIAF 2779
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                                                                                                                                                                                                                                                              797 YTEASYLHFPTFHAEFSADISFFRKTTALSGV -- FLENLGIKDFIRLEISSPSEITFAID 854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DIQHECNCDADKDEWTNDTGFLSF
                                                                                                                                                                           --TDTD------RSNSEAAWRIGPLRCYGDRRFWNAVSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin TITLE OF INVENTION: Fragments and Uses Thereof NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                               2671 OPSPLRNIPPFEGCIWNLVINSVPMDFARPVSFKNADIGRCAHOKLREDE----
----DGSEHCEQEVAYHCRRSRLLNTPDGTPFTWWIGRSNERHP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1024 SLSSSAIYTDSAPSKENIALSFVTTQAPSLLLFINSSSQDFV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25
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APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08460309
Patent No. 5837496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Engvall, Eva APPLICANT: Leivo, Ilmo
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                       QQC - - - ECGLDESCL
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STATE: California
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                                                                                                                                                                           KDHLPVTQIVI--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2382 ATRDLRDFMSVELTDGHIKVSYDLGSG-------MASVVSNQNHNDGKWKSFTLS 2429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2225 IDDSYWYRIVASRTGRNGTISVRALDGPKASIVPSTHHSTSPPGYTILDVDANAMLFVGG 2284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2334 QVED------SEGTIQFDGEGYALVSRPIRWYPNISTVMFKFRTFSSSALLMYL 2381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 ISLKFKSMQGDGVLFH-GEGQRGDHITLELQKGRLALHLNLGDSKARLSSSLPSATLGSL 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3111;
                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-UUL-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                    APPLICATION NUMBER: US/08/125,077 FILING DATE: 22-SEP-1993
           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3111 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
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TELECOMMUNICATION INFORMATION:
COMPUTER READABLE FORM:
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                                                                                                                                                                  CLASSIFICATION:
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Best Local Simi
Matches 224;
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2662 AVGHEQVDLDTCWLSERPKL-----APDAEDSKLLREPRAFFEGCVVDA----ALEYVP 2711
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APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3004 HTQSTSVDTNNPIYVGGYPAGVKQKCLRSQT----
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PROOF APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-UL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08125077
Patent No. 5872231
Patent No. 5872231 5840863
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MEDIUM TYPE: Floppy disk
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STREET: 4370 La Jol
CITY: San Diego
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCHNSIYEQSCEVYRHQGNTAGFFYIDSDGSGPLGPLQVYCNITEDKIWTSVQHNNTEL 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 MQCDGVLFH-GEGQRGDHITLELQKGRLALHLNLGDSKARLS-SSLPSATLGSLLDDQHW 269
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                                                                                                                APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
FILING DATE: 30-JAN-1990
PRIOR APPLICATION WITH A
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                                            2770 G-GRLHFMFDLGKGRTK--VSHPALLSDGKWHTVKTDYVKRKGFITVDGRESPMVTVVGD
                                                                                                                                        845 SPSEITFAIDVGNGPVELVVQSPSLLNDNQWHYVRAERNLKETSLQVDNLPRSTRETSEE
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-----YTEASYLHFP----TFHAEFSADISFFFKTTALSGV--FLENLGIKDFIRLEIS
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APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
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4370 La Jolla Village Drive, Suite 700
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SPSEITFAIDVGNGPVELVVQSPSLLNDNQWHYVRAERNLKETSLQVDNLPRSTRETSEE 904
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSE: Christens
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US-08-600-982-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2662 AVGHEQVDLDTCWLSERPKL-----APDAEDSKLLREPRAFPEQCVVDA----ALEYVP 2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 TSYSL-MFSDTGRNWKQYKQEDSIWT-FAGNMNADSVVHHKLLHSVRARFVRFVP---LE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 MQGDGVLFH-GEGQRGDHITLELQKGRLALHLNLGDSKARLS-SSLPSATLGSLLDDQHW 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 HXVLIERVG-----KQVNFTVDKHTQHFRTKGETDALDIDYE--LSFGGIPVPGKPGT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 VNSSGSYL--LLPGTPQIDGLSVSFQFRTWNKDGLL------LSTELSEGSGTLL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SVQQGSL----GNFSDLHIDLCSIKDRCLPNYCEHGGSCSQSWTTFYCNCSDTSYTG 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       581 ATCHNSIYEQSCEVYRHQGNTAGFFYIDSDGSGPLGPLQVYCNITEDKIWTSVQHNNTEL 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WNPSGKIG-----MRVEVYGCSYKSDV-ADFDGRSSLLYRFNQKLMSTLKDVISLKFKS 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 FLKK-----NFHGCIENLYYNGVNIIXLAKRKHQIYTVGNV--TFSCSEPQIVPITF 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRVRGANPEKPYAMALDYGGSMEQLEAVIDGSEHCEQEVAYHCRRSRLLNTPDGTPFTWW 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      470 -EAAPPAPDSTWVQIYSGNSYYFGGCPDNLTDSQCLNPIKAFQGCMRLIFIDNQPKDLI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 LSLEGGILRLVIQKMTERVAEILTGSNLNDGLWHSVSINARRNRITLTLDD------
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                                                                                                                                                                                                                                                                                                                                                           Length 3075;
                                                                                                                                                                                                                                                                                                                                                   Query Match 4.2%; Score 294; DB 2; L
Best Local Similarity 19.3%; Pred. No. 8.8e-17;
Matches 238; Conservative 178; Mismatches 474;
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                US-08-125-077-5
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2770 G-GRLHFMFDLGKGRTK--VSHPALLSDGKWHTVKTDYVKRKGFITVDGRESPMVTVVGD 2826
                                                                                                                                                                                                                                            956 GCPGHCSSYGSICHNGGKCVEKHNGYLCDCTNSPYEGPFCKKEVSAVFEAGTSVTYMFQE 1015
                                                                                                                                                                                                                                                                                                                  ------FD-GSGYAALVKE 2906
                                                                                                                                                                                                                                                                                                                                                                                                         1016 PYPVTKNISLSSSAIYTDSAPSKENIALSFVTTQAPSLLLFINSSSQDFVVVLLCKNGSL 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1119 --QQLRLSYN-----FSPEVEFRVIRSLTLGKVTENLGLDSEVAKANAMGFAGCM--- 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2948 KVLFHVNNGAGRITPAYEPKTATVLCDG----KWHTLQANKSKHRITLIVDGNAVGAESP 3003
                                                                                  GHFRLQLNSQLFVGGTSSRQK-----GFLGCIRSLHLNGQKMDLEERAKVTSGVRP
                                                                                                                                                             2827 GTM-LDVEGLFYLGGLPSQYQARKIGNITHSIPACIGDVTVNSKQLDKDSPVSAFTVNR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2907 GYKVQSDV------NITLEFRTSSQNGVLLGISTAKVDAIGLELVDG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1076 QVRYHLNK ------EETHVFTIDADNFANRRMHHLKINREGRELTIQMD-----
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B170 protein as translated from sequence
of FIGURES 15A-15F, and as shown also in FIGURES
19A-19R
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1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gil, Susanna A.
APPLICANT: Ryan, Maureen C.
TITLE OF INVENTION: Epillyrin, an Epithelial Ligand for TITLE OF INVENTION: Integrins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,982
FILING DATE: US-SEP-1994
CLASSIFICATION: 435
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1542	1028	1088	Oy 1148 L-GLDS       Db 1668 LTTLRI	RESULT 10 PCT-US94-10261A- ; Sequence 24, A	GENERAL INFOR  APPLICANT:  APPLICANT:  APPLICANT:	TITLE OF IN TITLE OF IN NUMBER OF S CORRESPONDE	ADDRESSEE STREET: CITY: Se STATE: W	COUNTRY:  ZIP: 981  COMPUTER RE  MEDIUM TY	COMPUTER: COMPUTER: COMPUTER: CORRENT APP.	C II or C	REGISTRAT TELECOMMUNI TELEPHONE	E G B E	TYPE: am TOPOLOGY: ; MOLECULE TY ; DESCRIPTI	; DESCRIPTI PCT-US94-10261A-	Query Match Best Local Sim Matches 241;	Qy 93 TQGRYG,       Db 699 TYGRTQ	Qy 142 KLLHSV : : Db 755 ELIQQA
Query Match Best Local Similarity 19.3%; Pred. No. 1.9e-13; Matches 241; Conservative 176; Mismatches 447; Indels 384; Gaps 62;	OY 93 TQGRYGSSDWVTSYSLMFSDJGRNWKQYKQEDSIWTFAGNMNADSVVHH 141	QY 142 KLLHSVR-AREVREVPLEWNPSGKIGMRVEVYGGSYKSDVADFDGRSSLLYRFNQKL 197 : :	Qy 198 MSTLKDVISLKFKSMQGDGVLFHGEGQRG-DHITLELQKGRLALHLNLGDSKARLSSSLP 256 ::	OY 257 SATLGSLLDDQHWHXVLIERVGKQVNFTVDKHTQHFRTKGETDAL 301 : ;	OY 302 DIDXELSFGGIPVPGK-PGTFLKKNFHGCIENLYYNGVNIIXLAKRRKHQIYTVGNV 357	QY 358 TFSCSEPQIVPITFVNSSGSYLLLPGTPQIDGLSVSFQFRTWNKDGLLLST 408	OY 409 ELSEGSGTLLLSLEGGILRLVIQKMTERVAEILTGSNLNDGLWHSVSINARRNRITLT 466	QY 467 LDDEAAPPAPDSTWVQIYSGNSYXFGGCPDNLTDSQCLNPIKAFGGCMRLIFIDNQPK 524  DD 1077 VDVQNTILDGEVFDFSTYXLGGIPIAIRERFNIS-TPAFRGCMKNLKK 1123	QY 525DLISVQQGSLGNFSDLHIDLCSIKDRCLPNYCEHGGSCSQSWTTFYCN 572   1   1   1   1   1   1   1   1   1	QY 573 CSDTSYT600 	OY 609 -SDGSGPLGPLQVXCNITEDKIWTSVQHNNTELTRVRGANPEKPYA 653	OY 654 MALDYGGSMEQLEAVIDGSEHCEQEVAYHCRRSRLLNTPDGTPFTWMIGRSNERHPYWGG 713 1	QY 714 SPPGVQQCECGLDESCLDIQHFCNCDADKDEWINDTGFLSFKDHLPVTQIVITDTDRSNS 773	Qy 774 EAAWRIG PLRCYGDRRFWNAVSFYTEASYLHFPTFH	OY 810AEFSADISFFFKTTALSGVFLENLGIKDFIRLEISSPSEITFAIDVGNGPVELVVOS 866 :: :  :  :  :  :  :     :	OY 867 PSLLNDNOWHYVRAERNLKETSLQVDNLPRSTRETSEEGHFRLQLNSQLFVGGTSSRQ 924 Db 1440 KEKCNDGKWHTVVFGHDGEKCRLVVDGIBAFGSLPGNSTTSTRAPVYGSPDRAFR 1497	925KGFLGCIRSLHLNGOKMDLEERAKVTSGVRPGCPGHCSSYG-SIC

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62;
                                                                                                                            DNFANRRMHHLKINREGRELTIOMDQOLRLSYNFSPEVEFRVIRSLTLGKVTEN 1147
HNGGKCVEKHNGYLCDCTNSPYEGPFCKKEVSAVFEAGTSVTYMFQEPYPVTKNISLSS 1027
                             VVLAHSVLL------GP----EFKLVFS-------IRPRSLTG 1573
                                                             SAPSKENIALSFVTTQAPSLLLFINSSSQDFVVVLLCKNGSLQVRYHLNKEETH 1087
                                                                                             SQPGKH------CKVTASMDSGAGGTS 1607
                                                                                                                                                  PE: protein
ON: E170 protein as translated from sequence of
ON: FIGURES 15A-15F, and as shown also in FIGURES 19A-19R
24
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ilarity 19.3%; Pred. No. 1.9e-13;
Conservative 176; Mismatches 447; Indels 384; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R-ARFVREVPLEWNPSGKIGMRVEVYGCSYKSDVADFDGRSSL---LYRFNQKL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSDWVTSYSLMFSDTGRN------WKQYKQEDSIWTFAGNM--NADSVVHH 141
                                                                                                                                                                                                                                                                                                                                      Carter, William G.
Gil, Susanna A.
Gil, Susanna A.
Ryan, Maureen C.
Ryan, Billigiln, an Epithelial Ligand for VERTION: Integrins
ENCURNES: 30
ENCE ADDRESS:
ENCE ADDRESS:
1420 Fifth Avenue
                                                                                                                                                                                          EVAKANAMGFAGCMSSVQYNHI-APLKAALRHATVAPVTVHG 1193
                                                                                                                                                                                                            24 pplication PC/TUS9410261A MATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ibelton, Dennis K.
TION NUMBER: 26,997
UCATION INFORMATION:
UE: (206) 682-8100
(206) 224-0779
FOR SEQ ID NO: 24:
HARACTERISTICS:
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370 -----LKEGEEDGFWCICADGFEGE------NCEVNVDDCEDNDCENNS--TCVDGIN 1014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1165 SYLQIPSAKVRPQTNITLQIATDEDSGILLYK-GDKDHIAVELYR-GRVRASYDTGSHPA 1222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 KDGLLLSTELSEGSGTLLLSLEGGILRLV----IQKMTERVAEILTGSNLN-----DG 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LWHSVSINARRNRITL-----TLDDEAAPPAP-----DSTWVQIYSGNSYYFGG- 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 GNVTFSCSEPQIVP-----ITFVNSSGSYLLLPGTPQ-----IDGLSVSFQFRTWN 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --C--PDNLTDSQCL-NPIKAF--QCCMRLIFIDNQPKDLISVQQGSLGNFSDLHIDLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  880 ARCAGPGEMADKLLLTTPSKKFTCQG------PVD------VNILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        589 EQSCEVYRHQGNTAGFFYIDSDG-SGPLGPLQVYCNITEDKIWTSVQHNNTELTRVRGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PEKPYAMALDYGGSM--EQLEAVIDGSEHCEQEVAYHCRRSRLLNTPDGTPFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1525;
1668 LTTLRIPUWKS---FFGCLRNIHVNHIPUPUFTEALE--VQGPVSLNG 1709
                                                                                                          Sequence 2, Application US/09191647

Sequence 2, Application US/09191647

GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Assier-Lavigne, Marc
APPLICANT: Essier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/191,647
CURRENT FILING DATE: 1998-11-13
EARLIER FILING DATE: 1998-11-14
EARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOFFWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.6%; Score 248; DB 3; L 22.3%; Pred. No. 4.4e-13; tive 95; Mismatches 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: human US-09-191-647-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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S-AIYSVETINDGNFHIVELLALDQSLSLSVDGGNPKIITNLSKQS--TLNFDSPLYVGG 1279
SYLOIPSAKVRPOTNITLQIATDEDSGILLYK-GDKDHIAVELYR-GRVRASYDTGSHPA 1222
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APPLICANT: Ense, Katja
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,153
CURRENT FILING DATE: 2000-03-31
PRIOR PILING DATE: 1998-11-13
PRIOR PILING DATE: 1998-11-13
PRIOR PLICATION NUMBER: 09/191,647
PRIOR PILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOOTWARE: Patentin Ver. 2.0
SEQ ID NO 2.
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Best Local Similarity 22.39
Matches 168; Conservative
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APPLICANT: Goodman
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; TYPE: PRT
; ORGANISM: human
US-09-540-153-2
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US-09-540-153-2
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                              861 ELVVQSPSLLNDNQWHYVRAERNLKETSLQVD-NLPRSTRETSEEGHFRLQLNSQLFVGG
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22.3%; Pred. No. 4.4e-13;
.1ve 95; Mismatches 286; Indels 206;
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APPLICANT: Brose, Katja
APPLICANT: Fessler-Lavigne, Marc
APPLICANT: Tessler-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT APPLICATION NUMBER: 60/065,544
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                     966 SICHNGGKCVEKHNGYLCDCTNSPYEGPFCKKEVS 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09540245A Patent No. 6270984 EMBRAL INFORMATION: APPLICANT: Goodman, Corey
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Best Local Similarity 22.33
Matches 168; Conservative
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                                                                                           -----FKCDCTPGYVGEHCDIDFDDCQDNKCKNGAHCTDAVNGYTCICPEGYSG 1104
                                                                                                                                                                                                                                                                                                                  1165 SYLQIPSAKVRPQTNITLQIATDEDSGILLYK-GDKDHIAVELYR-GRVRASYDTGSHPA 1222
                                                                                                                                                                                                                                                                                                                                                                           1105 LFCEFSPPMVLPRTSPCDNFDCQNGAQCIVRINEPICQCLPGYQGEKCEKLVSVNFINKE 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                589 EQSCEVYRHQGNTAGFFYIDSDG-SGPLGPLQVYCNITEDKIWTSVQHNNTELTRVRGAN 647
                                                                      -----PEKPYAMALDYGGSM--EQLEAVIDGSEHCEQEVAYHCRRSRLLNTPDGTPFT 698
                                                                                                                                                                                                                                                                                 801 SYLHFPTFHAEFSADISFFFKTTALSGVFLENLGIKDFIRLEISSPSEITFAIDVGNGPV 860
                                                                                                                                                                                                                                                                                                                                                      861 ELVVQSPSILINDNQWHYVRAERNIKETSLQVD-NLPRSTRETSEEGHFRLQLNSQLFVGG 919
                                                                                                                                                                                                                                                                                                                                                                                                                            ----TSSRQ-----KGFLGCIRSLHLNGQKMDLEERAKVTSGVRPGC-PGHCSSYG 965
                                                                                                                                        699 WWIGRSNERHPYWGGSPPGVQQCECGLD-ESCLD-IQHFCNCDADKDEWT----NDTG
                                                                                                                                                                                                             751 -FLSFKDH--LPVTQIVITDTDRSNSEAAWRIGPLRC-----YGDRRFWNAVS--FYTEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Valenzuela, et al.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS
TITLE OF INVENTION: NO LIGANDS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               966 SICHNGGKCVEKHNGYLCDCINSPYEGPFCKKEVS 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Regeneron Pharmaceuticals, Inc
STREET: 777 Old Saw Mill Road
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/644,271
FILING DATE: 10-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: USSN 60/008,657
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REG 195A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32, Application US/08644271
Patent No. 5814478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Cobert, Robert J
REGISTRATION NUMBER: 36,108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: RE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette
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US-08-644-271-32
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STATE: N
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      096 FANRRMHHLKINREGRELTIQMDQQLRLSYNFSP--EVEFRVIRSLTLGKVTENLGLDSE 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          987 NSPYEGPFCKK---EVSA-----VFEAGTSVTYMFQEPYPVTKNISLSSSAIYTDSAPS 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    775 AAWRIGPLRCYGDRRFWNAVSFYTEASYLHFPTFHAEFSAD-----ISFFFKTTALSGV 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GSGPF-----LADFNGFSHLELRGLHT-FARDLGEKMALEVVFLARGPSGL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             829 FLEN----LGIKDFIRLEISSPSEITFAIDVGNGPVELVVQSPSLLNDNQWHYVRAERNL 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 LLYNGQKTDGKGDFVSLALRD-RRLEFRYDLGKGAA--VIRSREPVTLGAWTRVSLERNG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 885 KETSLQVDNLPRSTRETSEE---GHFRLQLNSQLFVGGTSSRQK-----GFLGCIR 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :::|:| : || |: : || || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111 || |: 1111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 LVSLGGRQLLTPEHVLRQVDVTS-----FAGHPCTRASGHPCLNGASCVPREAAYVCLCP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 --TNRWLRVVAHREQREGSLQVGNEAPVT-GSSPLGATQLDTDGALWLGGLPE-LPVGPA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    715 PPGVQQCECGLDESCLDIQHFCNCDADKDEWTNDTGFLSFKDHLPVTQIVITDTDRSNSE 774
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT PILLING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOGTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 183
LENGTH: 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 PEGGAQCECPLGRE----GTFCQTASGQD-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
3.4%; Score 235.5; DB 2
Best Local Similarity 24.4%; Pred. No. 8.2e-13;
Matches 121; Conservative 71; Mismatches 193
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                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: Human Agrin
; LOCATION: 1...492
; OTHER INFORMATION:
US-08-644-271-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 LPKAYGTGFVGCLRDV 467
                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                      single
amino acid
                                                                STRANDEDNESS:
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US-09-188-930-183
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38;
                                                                                                                                                                                                                        165 CLSNPCKNDGTC-----SNPCKHGQDCDVPIHACT-----SNPCKHG 212
                                                                                                                                                                                                                                                                                               281 DFCAQDLNPCQHD------SKCILTPKGFKCDCTP--GYIG--------EH 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               560 GSC----SQSWTTFYCNCSDTSYTGATCHNSIYEQSCEVYRHQGNTAGFFYIDSDGSGP 614
                                                                                                                                                                                                                                                                                                                                              615 LGPLOVYCNITEDKIWTSVQHNNTELTRVRGAN-----PEKPYAMALDYGGSM--EQL 665
                                                                                                                                                                                                                                                                                                                                                                        250 ------C------ENNS--TCVDGINNYTCLCPPE------YTGELCEEKL 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CECGLDESCLD--IQHFCNCDADKDEWT----NDTG-FLSFKDHLPVTQIVITDTD--- 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: |: | | : : | 316 CDIDFDD-CQDNKCKNGAHCTDAVNGYTCVCPEGYSGLFCEFSP--PMVFLRTSPCDNFD 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      821 KTTALSGVFLENLGIKDFIRLEISSPSEITFAIDVGNGPVELVVQSPSLLNDNQWHYVRA 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             881 ERNLKETSLQVD-NLPRSTRETSEEGHFRLQLNSQLFVGG-----TSSRQ-----KG 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 927 FLGCIRSLHLNGQKMDLEERAKVTSGVRPGC-PGHCSSYGSICHNGGKCVEKHNGYLCDC 985
                                                                                                                                                                                                  503 CL-NPIKAFQGCMRLIFIDNQPKDL--ISVQQGSLGNFSDLHIDLCSIKDRCLPNYCEHG 559
                                                                                                                                                                                                                                                                                                                                                                                                                   666 EAVIDGSEHCEQEVAYHCRRSRLLNTPDG----TPFTWWIGRSNERHPYWGGSPPGVQQ 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               770 -RSNSEAAWRIGPLRC----YGDRRFWNAVS---FYTEASYLHFPTFHAEFSADISFFF 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.4%; Score 233.5; DB 4; Length 771; Best Local Similarity 23.4%; Pred. No. 2.8e-12; Matches 130; Conservative 73; Mismatches 191; Indels 161; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           986 TNSPYEGPFCKKEVS 1000
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; ORGANISM: Rat
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (717)...(717)
US-09-188-930-183
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Search completed: April 11, 2002, 16:39:38 Job time: 10590 sec

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/cgn2_6/ptodata/1/ina/backfiles1.seq:5258288-3 + 185.00 296.92 6.9e-09 326
/cgn2_6/ptodata/1/ina/5A_COMB.seq:0S-08-456-647B-19 + 181.50 290.98 1.5e-08
/cgn2_6/ptodata/1/ina/5B_COMB.seq:0S-08-237-401A-19 + 181.50 290.98 1.5e-08
/cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-936-135-1 + 180.50 290.71 1.5e-08
        186.50 302.16 3.5e-09 5.00 296.92 6.9e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin TITLE OF INVENTION: Fragments and Uses Thereof NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-460-309-1
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
            /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-936-135-3 +
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-UUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
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REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
; Sequence 1, Application US/08460309
; Patent No. 5837496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-460-309-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-770-643A-2 x US-08-460-309-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Engvall, Eva APPLICANT: Leivo, Ilmo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326.50
0.669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION:
US-08-460-309-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8378
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4765
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6585
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1934
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Sequence

Sequence

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(cgn2_6/prodate_1/
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2.6e-09
                                                                                                                                                                     About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/1na/5B_COMB.seq:US-08-658-340-1 +
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OM of: US-09-770-643A-2 to: Issued_Patents_NA:*
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Search time (sec): 108.390000
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Page 2

205 577	IleSerLeuLysPheLysSerMetGlnGlyAspGlyValLeuPheHis	220 626
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237 677	rgLeuAlaLeuHisLeuAsnLeuGlyAspSerLysAlaArgLeuSerSer :::::::::::::::::::::::::::::::::	253 720
254 721	SerLeuProSerAlaThrLeuGlySerLeuLeuAspAspGlnHisTrpHi :::       :::       : GAGTACCCAGATTGACTATTGATGACTCATATTGGTA	270 758
270 759	<pre>s***ValLeulleGluArgValGlyLysGlnValAsnPheThrValAsp. : ::::: :::   :::    CCGTATCGTAGCATCAAGAACTGGGAGAAATGGAACTATTCTGTGAGAG</pre>	286 808
287 809		293 858
294 859	ThriysGlyGluThrAspAlaLeuAspIleAspTyrGluLeuSe :::	308 908
308 909	rPheGlyGlyIleProValProGlyLysProGlyThrPheLeuLysLys.	324 940
325 941		33 <b>4</b> 990
335 991	TyrasnGlyvalasnIleIle***LeualaLysargArgLysHisGlnIl 	351 1035
351 1036	eTyrThrValGlyAsnValThrPheSerCysSerGluProGlnIleValP     ::: 	368 1075
368 1076	rolleThrPheValAsnSerSerGlySerTyrLeuLeuLeuProGlyThr        ATAGTGAGGGGACT	384
385	ProGln1leAspGlyAll	389 1139
390	GTACCCCAACATCTCCACTGTCAAGATTTTTTTTTCTTCAAGTACCCAACATCTCCACTGTCAAGTTCAAGAACATTTTCTTCAA	402 1189
402	spGlyLeuLeuLeuSer ::::	407 1239
408	ThrGluLeuSerGluGlySerGlyThrLeuLeuLeuSerLeuGluGlyGl .::	424 1289
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441	alSerIleAsn :::::::: rcACTCTGTCA	457 1353
458	AlaargargasnargileThrLeuThrLeu	467

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500	AspSerGlnCysLeuAsnProIleLysAlaPheGlnGlyCy     ::: :::    TTGAGTATGAAAGCAAGGCAGAAGTAAATCTGAAGAAATATTCGGGTG	513 1553
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530	InGlnGlySerLeuGlyAsnPheSerAspLeuHisIleAspLeuCysSer	546 1616
547	9ASPATGCYSLeuProAsnTyrCysGluHisGlyGlySerCysSe :::    :::    :::	563 1663
563	rGlnSerTrpThrThrPheTyrCysAsnCysSerAspThrSerTyrThrG :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::     :::     :::     :::	580 1683
580	lyAlaThrCysHisAsnSerIleTyrGluGlnSerCysGluValTyrArg:::            ::: 	596 1733
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r	TrpThrSerValGlnHisAsnAsnThrGluLeuThrArgValArgGlyAl	46
1792	· · · · · · · · · · · · · · · · · · ·	1808
646 1809	aAsnProGluLysProTyrAlaMetAlaLeuAspTyrGly	659 1858
660	GlySerMetGluGlnLeuGluAlaValIle	669
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722	.GluCysGlyLeuAspGluSerCysLeu	730

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994		. 697
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581	ATCCCCACCAAATCAATGATGGCCAGTGGCACAAGATTAAGAT	2624
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699		2718
914		926
719		2768
926		938
769		2818
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865		2893

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Sequence I. Application US/08125077

Sequence I. Application US/08125077

Patent No. 5872231 5840863

GENERAL INFORMATION:

APPLICANT: Edivol:

TITLE OF INVENTION: Fragments and Uses Thereof

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2970
                                                                        :::||| ::::: 2970 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2971 .....TTCGCGACAACTACAACGACTGGAGTTCTT 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3051 TGAAAAGTTGATGTTCATGTGGACAATGGTGGGGGGGGAGATTCACTGCTG 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ......LeuGlnValArgTyrHisLeuAsnLysGluGluThrHisVal 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3101 TCTATGATGCTGGGGTTCCAGGGCATTTGTGTGATGGACAATGGCATAAA 3150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1089 PheThrileAspAlaAspAsnPheAlaAsnArgArgMetHisHisLeuLy 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3151 GTCACT......GCCAACAAGATCAAACATGA 3182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1021 sAsnIleSerLeuSerSerSerAlaIleTyrThrAspSerAlaProSerL 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1105 sIleAsnArgGluGlyArgGluLeuThrIleGlnMetAspGlnGlnLeuA 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3233 CTACATCAGCTGACACAAATGACCCTGTGTTTGTTGGAGGCTTCCCAGAT 3282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3283 GACCTCAAGCAGTTTGGCCTAACAACCAGTATTCCGTTCCGAGGTTGCAT 3332
988 erProTyrGluGlyProPheCysLysLysGluValSerAlaValPheGlu 1004
                                                                                                                                                                                                                              1005 AlaGlyThrSerValThrTyrMetPheGlnGluProTyrProValThrLy 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1038 ysGluAsnIleAlaLeuSerPheValThrThrGlnAlaProSerLeuLeu 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1066 .....ValValLeuLeuCysLysAsnGlySer......1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-125-077-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1055 LeuPheIleAsnSerSerSerGlnAspPheVal.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATUR
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3333 CAGATCCCTGAAGCTCACCAAAGGCACA 3360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1136 eArgSerLeuThrLeuGlyLysValThr 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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CURRENT APPLICATION	V DATA:	
FILING DATE: 22-	_	
PRIOR APPLICATION D		
APPLICATION NUMBER: US PCT/US 9 FILING DATE: 21-SEP-1994	sR: US PCT/US 94/10730 SEP-1994	
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/4 FILING DATE: 30-JAN-1990	AATA: ER: US 07/472,319 JAN-1990	
PRIOR APPLICATION DA	DATA: ER: US 07/919,951	
FILING DATE: 27 - ATTORNEY/AGENT INFO	27-JUL-1992 INFORMATION:	
NAME: Campbell, Cat REGISTRATION NUMBER:	Cathryn A. BER: 31,815	
REFERENCE/DOCKET TELECOMMUNICATION I	NUMBER: P-LA 9721 INFORMATION:	
TELEPHONE: (619) TELEFAX: (619) 5	) 535-9001 535-8949	
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:	ID NO: 1: STICS:	
LENGTH: 3554 bas TYPE: nucleic ac	se pairs	
NDEDNESS: LOGY: line	single ar	
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104	.669 Gaps: 50 3.964 Percent Identity: 20.360	
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205 IleSerLeuLysPhe	IleSerLeuLysPheLysSerMetGlnGlyAspGlyValLeuPheHis	\(\bar{2}\)
-		979
		237
627 TGGAAGTGCCAAATT	TGGAAGTGCCAAATTTATTGACTTTCTGGCTATAGAAATGCGTAAAGGCA	929
237 rgLeuAlaLeuHisL ::::::: 677 AAGTCAGCTTCCTCT	rgLeuAlaLeuHisLeuAsnLeuGlyAspSerLysAlaArgLeuSerSer : :::::::::::::::::::::::::::::::	253 720
254 SerLeuProSerAla	rpHi	270
:::    :::     721 GAGTACCCAGATTTGACT	:::      ::::::    :::::::   :::::::::	
270 s***ValLeuIleGl		286
759 CCGTATCGTAGCATC	: ::::: ::::::::::::::::::::::::::::::	808
287		293
809 CCCTGGATGGACCCA	ACACCATTCGACG	858
	ThrLysGlyGluThrAspAlaLeuAspIleAspTyrGluLeuSe :::         :::	308
		806
	rPheGlyGlyIleProValProGlyLysProGlyThrPheLeuLysLys	324
STUDESTEEDING 606	c	940

325		334
941	CTGATGCTGTACGTGTG	066
335		351
991	TTTGACAACA	1035
351	eTyrThrV	368
1036		1075
368	rolleThrPheValAsnSerSerGlySerTyrLeuLeuLeuE	384
1076	AT	1089
385	ProglnIleAspGly	389
1090	ATTCAATTTGATGGAGGATTATGCATTGGTCAGCCGTCCCATTCGC	1139
390	LeuSerValSerPheGlnPheArgThrTrpAsn	402
1140	GTACCCCAACATCTCCACTGTCATGTTCAAGTTCAGAACATTTTCTTCG	1189
402	spGlyLeuLeu	407
1190	TITITITE GTGCTCTTCTGATGTATCTTGCCACACGAGACCTGAGAGATTTCAT	1239
408	ThrGluLeuSerGluGlySerGlyThrLeuLeuLeuSerLeu	424
1240	GTGGAGCTCACTGATGGGCACATAAAAGTCAGTTACGATCTGGGCTCAG	1289
424	ValileGlnLysMetThrGluAr	441
1290	AATGGCTTCGGT	1303
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1354	AATTCAAAAACAAGCCAATATATCAATTGTAGATATAGA	1403
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1404	AGGAGAATATAGCAACTTCGTCTTCTGGAAACAACTTTGGTCTT	1453
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1454	GAAAAGCAGATGACAAAATATTTTGGTGGCCTGCCAACGCTGAGAAAC	1503
200		513
1504	TTGAGTATGAAAGCAAGGCCAGAAGTAAATCTGAAGAAATATTCCGGCTG	1553
513	ĕ.	530
1554	CCTCAAAGATATTGAAGAACTCCGTACAATATACTGGTAGTC	1603
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1604	CCGATTATGTTGG	1616
547	CysGluHisGlyGlySerCy	563
1617	ACACAGTTAGCTTT	1663
563	TyrCysAsnCysSerAspThrSerTyrTh :::   :::	0
1664		1683

<pre>lyalaThrCysHisAsnSerIleTyrGluGlnSerCysGluValTyrArg 596 ::</pre>	His.GinGlyAsnThralaGlyPhePheTyrIleAspSerAspGlySerG 613     :::        :::   :::: ::        ::: CACCAAGAATGAGTCCGGCATCATTTTGGGAAGTGGAGGGACA. 1779	ouGlnValTyrCysAsnIleThrGluAspLysIle 629	rhrGlu		aAanProGluLysProTyrAlaMetAlaLeuAspTyrGly 659 :::			CATGATGGAAGAAGATTC 1943	aTyrHisCysArgArgSerArgLeuLeuAsnThrProAspGlyThrProP 697 :        :::   :::    :::     :: cGTTCATGTAGAGGCAACTAGAGTCTTTACAGTTCAAGTGGATGAA 1993	heThrTrpTleGlyArgSerAsnGluArgH1sPro 709	AAAACCTGACAGTTGAACAGCCTATCGAAGTTAAA 2043	- 0	SELECTICACTICAATTICAACTITCCCCACTCAG 2093	`		 TCCCCATGGACTTTGCAAGGCCTGTGTTCAAAAATGCTGACATTGGT 2193	HisPheCysasnCysAspalaAspLysAspGluTrpThrAsnAspThrGl 750 ::: ::::: :::::	AAACTCCGTGAAGATGAA2226	yPheLeuSerPheLysAspHisLeuProValThrGlnlleVallle 765	.GATGGAGCAGCTCCAGCTGAAATAGTTATCCAGC 2260		CTGAGCCAGTTCCCACCCCAGCCTTTCCTACGCCCACCCA	ArgSerAsnSerGlualaalaTrpArgIleGlyProLe 782	SCAGAATCAGAACCAGCTCTTTGATAGGGAGCAA 2360	79	24	laAsp 815	ACCGTCTCACAATTGAGTTGGAA2445
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580	597 1734	613 1780	630	1792	646	660	670	1909	680	697	1994	710	7 2 2	a o	731	2144	734	2194	750	2227	166	2261	770	2311	7.8	ဖ	799	7007

2446	:::               ::: GTAAGAACCGAATCCGGCTTGCTTTTACAT 2483
830	uGluAsnLeuGlyIleLysAspPheIleArgLeuGluIleSerSerProS 847 : ::::::        ::::::: ::: GGCTGCGATCAATCATGCTGATTTTGCAACAGTTCAGCTGAGAAATGGAT 2533
847	erGluileThrPheAlaileAspValGlyAsnGlyProValGluLeuVal 863    :::    :::     ::::: ::: TGCCCTACTTCAGCTATGACTTGGGGAGACGCGACACCCACCATG 2580
864	ValGinSerProSerLeuLeuAsnAspAsnGinTrpHisTyrValArgal 880 :::
880	aGluArgAsnLeuLysGluThrSerLeuGlnValAspAsnLeuProArgS 897
897	ά ö
914	GlnLeuPheValGlyGlyThrSerSerArgGlnLysGl 926 :::   :::
926	yPheLeu
938	1yGlnLysMetAspLeuGluGluArgAlaLysValThrSerGlyValArg 954
955	ysProGlyHisCysSerSerTyrGlySerIleCysHisAs;        ::   TCCAGCTTCCATGT
971	ysCysValGluLysHisAsnGlyTyrLeuCysAspC. 
988	ysLysGluValSerAlaV        ::::: TTGCCAAAGCAGTTGGTGGA.
1005	AlaGlyThrSerValThrTyrMetPheGlnGluProTyrProValThrLy 1021 :::    :::::      :::   GTGGGATTGGACCTTCTTGTAGAATTTGAA
1021	MaileTyrThrAspSerAlaProSer
2970	2970
1038	nlleAlaLeuSerPhevalThrThrG    :::       TTCGCGACAACTA
1055	leasnSer:   :::    rcagragr
1066 3051	TGAAAAGTTGATGTTCATGTGGACATGGTGGGGGGGAATTCACTGCTG 3100
1075	LeuGlnValArgTyrHisLeuAsnLysGluGluThrHisVal 1088
08	ThrileAspAlaAspAsnPheAlaAsnArgArgMetHisHisLeuLy 110

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UNGLYARGGILGEUTHILGGINMETASPGINGINEGUA  INGIGAAGCAGGTGGAAGCCCAAAGCCCAAACCCAGGAT  INGIGAAACCAGGTGGAAGCCCAAAGCCCAAACCCAGGAT  TYCASAAPACACACCATTTGTAGAGGCTTCCCAGAT  TYTASNPheSerProGluValGluPheArgValii  TYTASNPheSerProGluValGluPheArgValii  TYTASCTACCAAAGCCCTGTTTGTTGTAGAGGTTCCCAGAT  TYTASCTACCAAAGCCAACCAGTTTCCGTTCCGAGGTTGCAT  TALL EVA;SANES, JOSHUA  ALL, EVA;SANES, JOSHUA  ALL, EVA;SANES, JOSHUA  ALCES: 4  TON DATA: WHERE: 387, 689  WHERE: 387, 6														
151 GTCACT. 105 SILEAST 105 SILEAST 1183 GCTCACY 122 TGLEUSE 123 CTACATC 125 136 EAR SSET 136 EAR SSET 137 CACATC 137 CACATC 138 EAR SSET 139 CACATC 139 CACATC 130 CACATC 131 CTACATC 131 CTACATC 131 CTACATC 132 CTACATC 133 CACATC 134 EARL 14                 14             15		333	LeuThrLeuGlyLysValThr 1145                       :CTGABGCTCACCAAGGCACA 3360	.6/ptodata/1/ina/backfiles1.seq:5444158-1	ock: MLL, EVA;SANES, JOSHUA LON: MEROSIN, NUCLEIC ACIDS THEREOF CES: 4 ION DATA: NHBER: US/08/87,642 N DATA: N DATA: NBER: 587,689 NHBER: 587,699 NHBER: 472,319	326.50 Length: 0.657 Gaps: 45.430 Percent Identity:	5444158-1	5444158-1 from: 1 to:						
		1125	1136 eArgSerL          3333 CAGATCCC	ame: /cgn2_6	documentation, and No. 5441 APPLICANT: E APPLICANT: E APPLICANTO SMENTS AND US NUMBER OF SE UNRERN APPLICATIO FILING DAT FILING DAT FILING DAT FILING DAT APPLICATIO FILING DAT ID NO:1: LENGTH: 35	lignment_scores: Quali Rat Percent Similari	ment_block: 9-770-643A-2	Align seg 1/1 t	205 IleSerLe     :: 577 ATTGTTGT	221 .GlyGluG    :::: 627 TGGAAGTG	237 rgLeuAlai ::::::: 677 AAGTCAGC	254 SerLeuPro ::: 721 GAGTACCO	270 s***Valld : ::: 759 CCGTATCG	287

294	ThrLysGlyGluThrAsp ::: TCTCCTCCAGGGTACACG	308
ō ō	rPheGlyGlyIleProValProGlyLysProGlyThrPheLeuLysLys 	9 4
325		334
335 991	TyrasnGly	351 1035
351	eTyrThrValGlyAsnValThrPheSerCysSerGluProGlnIleVal:	368 1075
368	rolleThrPheValAsnSerSerGlySerTyrLeuLeuLeuProG   AT	384 1089
89 60	ProglatleaspGlyarililil artcaatttgatggagaaggttatgcattggtcagccgtcccattcg	89
390	GTACCCCAA	402
402	spGlyLeuLeu	407
408	ThrGluLeuSerGluGlySerGlyThrLeuLeuLeuSerLeu :::       :::::    GTGGAGCTCACTGATGGGCACATAAAAGTCAGTTACGATCTG	424 1289
1290	ylleLeuArgLeuValIleGlnLysMetThrGluAr     A	441 1303
441	rGlySerAsnLeuAsnAspGlyLeuTrpHisSerValSerI ::::::                             CAATCAAAACCATAATGATGGGAAATGGAAATCACTC	457 1353
458	AlaargargasnargileThrLeuThrLeu	467 1403
468	<pre>spgluAlaAlaProProAlaProAspSerT :::    ::: :::: \ATATAGCAACTTCGTCTTCTGGAAACAACT</pre>	483 1453
483	snSerTyrTyrPheGlyGlyCysProAspAsn :::::              :ACAAAATATATTTGGTGGCCTGCCAACGCTG	499 1503
500	AspSerGlnCysLeuAsnPro	513 1553
513 1554	JLeullePhelleAspAsnGlnProl :        :::::   } \GATATTGAAATTTCAAGAACTCCGT	530 1603
53	InGlySerLeuGlyAsnPheSerAspLeuHisIleAspLeuCysSe	46
1604	rra rgCysLeuProAsnTyrCysGluHisGlyGlySe	1616 563

1617	:::    :::   :::  raccaaagaargticctggagaargtitacacagtiagctitc	1663
563	rGlnSerTrpThrThrPheTyrCysAsnCysSerAspThrSerTyrThrG :   :::	580 1683
580	1yAlaThrCysHisAsnSerIleTyrGluGlnSerCysGluValTyrArg ::	596 1733
597 1734	H1s.GlnGlyAsnThrAlaGlyPhePheTyrIleAspSerAspGlySerG	613 1779
613	lyproLeuGlyProLeuGlnValTyrCysAsnIleThrGluAspLysIle 	629 1791
630	TrpThrSerValGlnH18AsnAsnThrGluLeuThrArgValArgGlyAl	646
1792		1808
646 1809	aAsnProGluLysProTyralaMetalaLeuAspTyrGly	659 1858
099		699
1859		1908
670	GAGCCGAATCTGTTTCATGATGAAGAGAAAT	680 1943
680	ОР	697
1944		1993
697	heThrTrpTrpIleGlyArgSerAsnGluArgHisPro	709 2043
710		721
2044	AAGCTTTCGTTGGGGGTGCTCACCTGAATTCAACCTTCCCCACTCAG	2093
722	.GluCysGlyLeuAspGluSerCysLeu	730
2094		2143
731	mood a manage of the contract	733
734		750
2194	CCCTGTGCCCATCAGAAACTCCGTGAAGATGAA	2226
750	yPheLeuSerPheLysAspHisLeuProValThrGlnIleValIle 7	765
2227		2260
992	ThraspThrasp7	692
2261		2310
	ArgSerAsnSerGlualaAlaTrpArgIleGlyProLe	82
2311		m i
782	uArgCysTyrGlyAspArgArgPheTrpAsnAlaValSerPheTyrThrG 7	667

236	1 GCAGTTCGGGCTTTCAAGAAACAGTCACATTGCAATTGCATTTGATG	2407
79	9 luAlaSerTyrLeuHisPheProThrPheHisAlaGluPheSerAlaAsp	815
240		2445
81	6 IleSerPhePheLysThrThrAlaLeuSerGlyValPheLe	830
244	6GTAAGAACCGAAGCTGAATCCGGCTTGTTTTACAT	2483
83	0 uGluAsnLeuGlyIleLysAspPheIleArgLeuGluIleSerSerProS	847
248	4 GCCTCGCATCAATCATGCTGATTTTGCAACAGTTCAGCTGAGAAATGGAT	2533
84	7 erGluIleThrPheAlaIleAspValGlyAsnGlyProValGluLeuVal	863
253	4 TGCCCTACTTCAGCTATGACTTGGGGAGTGGGGACACCCACCATG	2580
98	4 ValGlnSerProSerLeuLeuAsnAspAsnGlnTrpHisTyrValArgAl	880
258	1 ATCCCCACCAAAATCAATGATGGCCAGTGGCACAAGATTAAGAT	2624
88	0 aGluArgAsnLeuLysGluThrSerLeuGlnValAspAsnLeuProArgS	897
262	5 AATGAGAAGTAAGCAAGAAGGAATTCTTTATGTAGATGGGGCTT	2668
89	7 erThrArgGluThrSerGluGluGlyHisPheArgLeuGlnLeuAsnSer	913
266	CCAACAGAACCATCAGTCCCAAAAAAGCCGACATCCTGGATGTCGTGGGA	2718
91	4 GlnLeuPheValGlyGlyThrSerSerArgGlnLysGl	926
271	9 ATGCTGTATGTTGGTGGGTTACCCATCAACTACACTACCGGAAGAATTGG	2768
92	6 yPheLeuGlyCysIleArgSerLeuHisLeuAsnG	938
276	9 TCCAGTGACCTATAGCATTGATGGCTGCGTCAGGAATCTCCACATGGCAG	2818
93	8 lyGlnLysMetAspLeuGluGluArgAlaLysValThrSerGlyValArg	954
281	9 AGGCCCCTGCCGATCTGGAACCCACC	2847
6	<pre>5 ProGlyCysProGlyHisCysSerSerTyrGlySerIleCysHisAsnGl                                      </pre>	71
284	8CATGTTG.	2864
6 6	1 yGlyLysCysValGluLysHisAsnGlyTyrLeuCysAspCysThrAsnS	88
286	5 GACATGTTTGCAAATGCTCAGAGGGGAA	80 O
96 88	8 erProTyrGluGlyProPheCysLysLysGluValSerAlaValPheGlu ::::::              ::::        :::	1004
	5 AlaglyThrSerValThrTvrWetPheGlnGlnProTvrProValThr[v	02
294	:::   ::::::	66
102	1 sAsnileSerLeuSerSerAlalleTyrThrAspSerAlaProSerL	1038
299	:::::    ::: :::::::::::::::::::::::::	3022
103	8 ysGluAsnIleAlaLeuSerPheValThrThrGlnAlaProSerLeuLeu	1054
302	3 TGGATGGAATGGTATTGAATGATTGATGAAAAGTTGATG	3063
105	5 LeuPheIleAsnSerSerGlnAspPheValValValLeuLeuCysLy	02
306,	4 TITCATGTGGACAATGGTGCGGGCAGATTCACTGCTGTCTAT	3105
1071	SASnGlySerLeuGlnValArgTyrHisLeuAsnLysGluGluThrHisV :::	1088
010	GATGCTGGGGTTCCAGGCCATTTGTGATGGACAATGGCATA	3140

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1942 ACAGCAAACCCTGAATATTGTGACAGT.....1968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2059 TGCAAAGAGCATGGTCAGAAAGGCCAACGACATCACAGATGAGATTCTGG 2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2009 GATGGTCTTCATGGGATACAGAGGGGTGATATTGATGCTATGATCAGTAG 2058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :::::|||::::
2170 GAACGAAGACTTC.....AAAAAGGCTCTGACTGATGCAGATAACTCGG 2213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2264 ATCAACCAACAGCTGTTGCCCTTGGGAAACATCTCTGACAACATGGACAG 2313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2402 CGACTG......CCAAATGACCTGGAAGATTGAAAGGATA 2436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2437 TACATCTCTGTCCTTGTTTCTCCAAAGGCCCAACTCAAGAGAAAATGGGG 2486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2109 ATGGGCTCAACCCC....ATCCAGACAGAT 2134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2314 AATA.....CGAGAACTAATTCAGCAGGCCAGAGATGCTGCCAGTAAGG 2357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2358 TTGCTGTCCCCATGAGGTTCAAT .....GGTAAATCTGGAGTCGAAGTC 2401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 rgAsn.....TrpLysGlnTyrLysGln 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 GluAspSerIleTrpThrPheAlaGlyAsnMet.....AsnAlaAspSe 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 rgPheValProLeuGluTrpAsnProSerGlyLysIleGlyMetArgVal 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 GluValTyrGlyCysSerTyrLysSerAspValAlaAspPheAspGlyAr 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 gSerSerLeu.....LeuTyrArgPheAsnGlnLysLeuMetSerT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 rValValHisHisLysLeuLeuHisSerValArg...AlaArgPheValA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 hrLeuLysAspVallleSerLeuLysPheLysSerMetGlnGlyAspGly 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 ValLeuPheHisGlyGluGlyGlnArgGly...AspHisIleThrLeuGl 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 uLeuGlnLysGlyArgLeuAlaLeuHisLeuAsnLeuGlyAspSerLysA 249
                                                                                                                                                                                                                                                                  24 ThralaThrAsnTyrAsnCysAspAspProLeuAlaSerLeuLeuSerPr 40
                                                                                                                                                                                                                                                                                                                                                                            40 oMetAlaPheSerSerSerSerAspLeuThrGlyThrHis...SerProA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 .....ArgValGlyThrGl 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 y.GlyTrpSerProAlaAspSerAsnAlaGlnGlnTrpLeuGlnMetAsp 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 LeuGlyAsnArgValGluIleThrAlaValAlaThrGlnGlyArgTyrGl 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2487 GTACTGAGAATATGTTT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 laGlnLeuAsnTrp.....
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Gaps: 67
Percent Identity: 19.713
                                                                                                                                                                                                            gn seg 1/1 to: US-08-600-982-23 from: 1 to: 5496
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0.428
44.789
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Ratio:
Cent Similarity:
nment_scores
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266	1s***ValLeuIleGluAr 	
281 2683	TATCAGTTTGCAAGGCTTAATTACACAAAGGAGCCACATCCAGTAAAC 2732	
292 2733	heArgThrLysGlyGluThrAspala 300 	
301 2783	LeuAspIleAspTyrGluLeuSerPheGlyGlyIleProVa 314    :::::         ::  CTTAATTTGGATCCTGAAATGTTGTATTTATGTTGGAGGTTACCCACC 2832	•
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330	leGluAsnLeuTyrTyrAsnGlyValAsnIleIle***LeuAlaLysArg 346                   ::  TrGAATTAGATGACCTCAATGAAAATGTTCTGAGCTTGTACAACTTC 2929	
347	ArgLysHisGlnIleTyrThrValGlyAsnValThrPheSerCysSerGl 363 :::	
363 2953	Prolle      CTTGTAGAAGGA	
371 3003	heValAsnSerSerGlySerTyrLeuLeuLeuProGlyThrProGlnIle 387 :: ::::::	
388 3050	AgpGlyLeuSerValSerPheGlnPheArgThrTrpAsnLysAspGlyLe 404 ::: :: :: :: ::	
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421		
438	AlaGluIleLeuThrGlySerAsnLeuAsnAspGlyLeuTrpHisSerVa 454	
454	SerileasnalaargargasnargileThrLeuThrLeuAspaspGlua 471	
471	laAlaProProAlaProAspSerThrTrpValGInIleTyrSerGlyAsn 487 :: ::::::::::::::::::::::::::::::::::	
488	SerTyrTyrPheGlyGlyGy9ProAspAsnLeuThrAspSerGlnCysLe 504 :::	
504	uAsnProlleLysAlaPheClnGlyCysMetArgLeullePhelleAspA 521	

338	5 TTCTACGCCTGCTTTCCGAGGCTGCATGAAAA	3416
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3417	ATTGAAGAAAACCAGTGGTGTCGTTAGATTGAATGATACTGTGGGGAGT	3466
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3467	7 ACCAAA	3472
546	ıProAsnTyrCysGluH	563
347	3AAGTGCT	3479
563	3 erGlnSerTrpThrThrPheTyrCysAsnCysSerAsp	575
348(		3529
576	ThrserTyrThr	579
3530		3579
580	)GlyAlaThrCysHisAsnSerI	287
3580		3629
587	leTyrGluGlnSerCysGluValTyrArgHisGlnGlyAsnThrAlaGly	603
3630		3667
604	Phe	615
3998		3711
. 616	6GlyProLeuGln.ValTyr.CysAsnIl	624
3713	2 ATCTCCACAGACGTATATGGATGGTTTACTGCATTATGTATCTGTAAT	3759
624	4 eThrGluAspLysIleTrpThrSerValGlnHis.AsnAsnThrGluLeu	640
376(	0AAGCGACAACTCTGGACTACGGCTTCTCATCGATGACCAGCTTCTG	3805
64]	1 ThrArgValArgGlyAlaAsnProGluLysProTyrAlaMetAlaLeuAs	657
3806	AGAAATAGCAAAAGGCTAAAACACATTTCAAGTTCCCG	3855
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3826	6 rcredecegeaaccAATTTGAGG	3878
149	4 isCysGluGluValAlaTyrHisCysArgArgSerArgLeuLeuAsn	069
387	:	3916
69	ThrProAspGlyThrProPheThrTrpTrpIleGlyArgSerAsnGluAr	707
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707	gHisProTyrTrpGlyGlySerPr	724
3956		3980
724	1 JyLeuAspGluSerCysLeuAspIleGlnHisPheCysAsnCysAspAla	740
398]	1 GTTTAAACAAA	3991
74]	1 AspLysAspGluTrpThrAsnAspThrGlyPheLeuSerPheLysAspHi	757
3991		3991
757	sLeuProValThrGlnIleValIleTh	774
3992	•	4037

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77	lualaalaTrpargIleGlyProLeuArgCys	84
4038	CCAAGACTTTTCGTATCAACCAGCTGTTGCAGGACACACCAGTGGCCTCC	4087
785	TyrGlyAspArgPheTrpAsnAlaValSerPheTyrTh 7 :::	798
798		809 4187
810		813
4188	TGCTATTCAAGCTTCCTCAGGAGCTGCTGAAACCCAGGTCACAGTTTGCT 4	237
814 4238	AlaAspIleSerPhePheLysThrThrAlaLeuSerGlyValPheLe 8 :::        :::	.30 275
830 4276	pPhelleArgLeuGlulleSerSerPros 8	47 322
847	erGlulleThrPheAlalleAspValGlyAsnGlyProValGluLeuVal 8	63
4323	GACGTCTGGTCTTTGCACTGGGGACAGATGGGAAAAATTGAGG 4	366
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880 4417	aGluArgAsnLeuLysGluThrSerLeuGlnValAspAsnLeuProArgS 8: ::::: ::::::::::::::::::::::::::::	897 4460
897	erThrargGluThrSerGluGluGlyHisPheArgLeuGlnLeuAsnSer 9 :::	13 510
914		924 4560
925 4561		941 4610
941	etAspLeuGluGluArgAlaLysValThrSerGlyValArgProGlyCys 9: :: ::	957 4657
958 4658	ProGlyHisCysSerSerTyrGlySerIleCysHisAsnGlyGlyLysCy 9	974 4701
974 4702	CysThrAsnSerProTyrG 9	991 4726
991 4727	ValPheGluAlaGlyThr        :::  GTTTTCAGC	1007 4753
1008	InGluProTyrProValThrLysAsnIleSe ::	1024 4767
1024	<pre>sralaileTyrThrAspSeralaProSerLysGluAsni    :::          :::   ::: rcctaAracacarcgGaAGTCACCCGGGAAGCAC</pre>	1041 4813

TOT	T TERTATEGRAFINE VALINITION OF THE TOOK TEATHER TOOK
481	4TATGTGTTTACCTG 4828
105	8 AsnSerSerGlnAspPheValValValLeuLeuCysLysAsn
482	9 GAGGCAGGAAA 4839
107	4 rLeuGlnValArgTyrHisLeuAsnI::::::::::::::::::::::::::::::::::::
. 0	lobenalabenahonDhom abenbrahorMotHieHieHieInulveI]
י ס	CACCAAAGCAGTCTCTGTGATGAACAGTGGCACTCGGTGGCAGTCGCC 493
10	8 ArgGluGlvArgGluEeuThrIleGlnMetAspGlnGlnDeuArgLeuSe 112
494	0 ATAAAACAACATCCTGCACCTGGAACTGGACACAGACAGTAGCTACAC 498
112	4
4990	
114	1 euGlyLysvalThrGluAsnLeuGlyLeuAspSerGluValAlaLys.1156
#OC.	JIGGAGGIGCICCAGCCAAIIIGACGACACIGAGGAICCCIGIGIGGGAAA 300
1157 5090	A AlaasnalaMetGlyPhealaGlyCysMetSerSerValGlnTyrAsnHi 1173 :::
117	3 sileAlaProLeuLysAlaAlaLeuArgH
512	
118	9 alThrValHisGly 1193   :::::::    2 TCAGTCTGAATGGT 5185
sed_name:	>: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:PCT-US94-10261A-23
Ø,	documentation_block: Requence 23, Application PC/TUS9410261A
	FLICANT: Carter, William G.
, API	PLICANT: Ryan, Maureen C. FLE OF INVENTION: Epiligrin, an Epithelial Ligand for
	rLE OF INVENTION: Integrins ABER OF SEQUENCES: 30
පි	CORRESPONDENCE ADDRESS: ADDRESSEE: Christensen O'Connor Johnson, and Kindness
	1420 Fifth Avenue
	CIII: Seattle STATE: WA
	COUNTRY: USA ZIP: 98101-8100
	COMPUTER READABLE FORM:
	uisk patible
	SYSTEM: Patent
CMI	RRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/10261A
	EP-1994
AT	NFORMATIO
	NAME: SNEICON, Dennis K. REGISTRATION NUMBER: 26,997
TEI	TELECOMMUNICATION INFORMATION: TELECOMMUNICATION:
	FELTERAX. (200) 00% 0100

AMAGEMENT   AMAG	15F															
	: 23: S: Lrs mrna e of cDNa to 3EpA cDNA; see FIGURES 15A-	ty: 254.00 Length: 132 10: 0.428 Gaps: 6 ty: 44.789 Percent Identity: 19.71	x PCT-US94-10261A-2	from: 1 to: 549	24 ThralaThrasnTyrasnCysAspAspProLeualaSerLeuLeuSerPr 40	40 oMetAlaPheSerSerSerSerAspLeuThrGlyThrHisSerProA     ::	56 laGlnLeuAsnTrp	TGCAAAGAGCATGGTCAGAAAGGCCAACGACATCACAGATGAGGTTCTGG	y.GlyTrpSerProalaAspSerAsnAlaGlnGlnTrpLeuGlnMetAsp 81   1   1   1   1   1   1   1   1   1	LeuGlyAsnArgValGluIleThrAlaValAlaThrGlnGlyArgTyrGl 98 ::: :::   :	ySerSerAspTrpValThrSerTyrSerLeuWetPheSerAspThrGlyA 115 :::::   ::::   :::::   GAACGAAGACTTCAAAAGGCTCTGACTGATGATGAGATAACTCGG 221	rgasntrplysglnTyrLysGln 122       :::::  TGAaTaAGTTAACCAACAACTACCTGATCTTTGGCGCGAAGATTGAAAGT 226	123 GludspSerIleTrpThrPheAlaGlyAsnMetAsnAlaAspSe 137 :::::	137 rValValHisHisLysLeuLeuHisSerValArgalaargPheVala 153 :::::::::::::::::::::::::::::::::::	153 rgPheValProLeuGluTrpAsnProSerGlyLysIleGlyMetArgVal        ::::::      TTGCTGTCCCCATGAGGTTCAATGGTAAATCTGGAGTCGAAGTC	170 GluvaltvrGlvCvsSerfivrEvsSerAenValalaaenDheaenGlvar 186

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186	gSerSerLeuLeuTyrArgPheAsnGlnLysLeuMetSerT	200
40,4	CI CCAAGGCCCCAACI CAAGAGAAAA	0
∾ .	hrLeuLysAspValIle	16
2487	GTACTGAGAATATGTTT	2503
217	ValLeupheHisGlyGluGlyGlnArgGlyaspHisIleThrLeuGl	232
232	uLeuGlnLysGlyArgLeuAlaLeuHisLeuGlyAspSerLysA	249
2554	AGTTGTGGATGGCCAGCTCACGTGTCTACAACCTGGGGGACCGTGAGG	2603
249	laArgLeuSerSerLeuProSerAlaThrLeuGlySerLeuLeuAsp   :::   :::      Grosaccaa	265
26	AspGlnHisTrpHis***ValLeuIleGluArqValGlyLysGln	80
2633	::::::	2682
281	ValAsnPheThrValAspLysHisThrGlnHisP	292
2683	:::!!! ATCAGTTTGCAAGGCTTAATTACACCAAAGGAGCCACATCCAGTAAA	2732
292	sGlyG	300
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301	LeuaspileaspTyrGluLeuSerPheGlyGlyIleProva     ::::::	314
314	LeuLysLysAsnPheHisGlyCy	330
. 2833	TGATTTTAAACTTCCCAGTCGACTAAGTTTCCCTCCATACAAAGGTTGTA	2882
330	leGluAsnLeuTyrTyrAsnGlyValAsnIleIle***LeuAlaLysArg 	346 2929
34	isGlnIleTyrThrValGlyAsnValThrPheSerCysSer	63
m	\ACATTCAATC	σ
36	uProGlnIleValProllerhrP	7.1
Ω.	aagtggagccttgtagaaggaaggaaggaagtcagac	_
371	heValAsnSerSerGlySerTyrLeuLeuLeuProGlyThrProGlnIle	387
) (		;
3050	AspGlyLeuSerValSerPheGLnPheArgThrTrpAsnLysAspGlyLe ::: ::: ::    CCCATCCCAACCTTTGGACAGACAATTCAGACCACCGTGGATAGAGGCTT	404 3099
404	uSerGluGlySerGlyThrLe	421
3100		3143
42	LuArgV	37
4	AGAAGATGGCAAGCTCATGGTGAGATACAAACTGAATTCAG	⊣ :
438	AlaGluIleLeuThrGlySerAsnLeuAsnAspGlyLeuTrpHisSerVe	454

9.	AAAGAGAGAGTTGGAGACGCCATAAACAACGGCAGAGACCATTCGAT	3243	
154	SerIleasnalaargargasnargIleThrLeuThrLeuAspaspGlua	471 3293	
171	laAlaProProAlaProAspSerThrTrpValGInIleTyrSerGlyAsn::    :::::::::::::::::::::::::::::::	487 3334	
35.	SerTyrTyrPheGlyGlyCysProAspAsnLeuThrAspSerGlnCysLe:::	504	
85	uAsnProlleLysAlaPheGlnGlyCysMetArgLeullePhelleAspA ::::	521 3416	
17	snGlnProLyssspLeulleSerVal 	529 3466	
30		546 3472	
73	Sercyss	563	
80	erGlusertrpThrThrPheTyrCysasnCysSerAsp 	575 3529	
30	Thrsertyrthr	579	
8 8	GlyAlaThrCysHisAsnSerI       ::::: ATTTGGATTTCAACCTTTCAACCCAGTGGCATATTAGATCATCAGA	587	
30	leTyrGluGInSerCysGluValTyrArgHisGlnGlyAsnThrAlaGly ::: :::::    CATGGACAAGGAACCTGCAGGTCACTCTGGAAGATGGT		
0.4 68		615 3711	
16		624 3759	
24	eThrGluAspLysIleTrpThrSerValGlnHis.AsnAsnThrGluLeu :: :::::      :::::         :::::     ::::     ::::	640 3805	
41	ThrArgvalArgGlyAlaAsnProGluLysProTyrAlaMetAlaLeuAs ::: :: :: :::         AGAAATAGCAAAAGGCTAAAACACATTTCAAGTTCCCGGCAGTCTCTGCG	657 3855	
57	pTyrGlyGlySerMetGluGluLeuGluAlaValIleAspGlySerGluH            TCTGGGCGGGAGCAATTTTGAGG	674 3878	
74		690 3916	
91	ThrProAspGlyThrProPheThrTrpTrpIleGlyArgSerAsnGluAr :::    :::	707 3957	

2 ,	ghiskiolyliipelyelyserkiokioelyvaleine	4 6
3958	AGATGTCCCTGGGAGGC	3980
724	uAspIleGlnHisPheCysAsnCysAsp	740 3991
741	pLysAspGluTrpThrAsnAspThrGlyPheLeuSerPheLysAspH	
3991		3991
757	LeuproValThrGlnlleVallleThrAspThrAspArgSerAsi     	774
ן ח		
774	lualaalaTrpargIleGlyProLeuArgCys ::::::      ::: CCAAGACTTTTGTATCAACCAGTGTTGCAGGACACACCAGTGGCTCC	784 4087
785	spArgArgPheTrpAsnAlaValSerPhe	198
4088	CCAAGGAGCGTGAAGGTGTGCCAAGACTTGCTCACCACTTCCCAAGAC	4137
798	rGluAlaSerTyrLeuHisPheProThrPheHis.	608
4138	CCAGGCCAATCATGGAGCCCTCCAGTTTGGGGACATTCCCACCAGCCACT	4187
810	AlaGluPheSer	813
4188	GTTTGC	4237
814	AlaAspIleSerPhePhePheLysThrThrAlaLeuSerGlyValPheLe	830
4238	TGGT	4275
830	uGluAsnLeuGlyIleLysAspPheIleArgLeuGluIleSerSerProS	847
4276	AAA	4322
847	erGlulleThrPheAlaIleAspValGlyAsnGlyProValGluLeuVal	863
4323	STCTGGTCTTTGCACTGGGGACAGATGGGAAAAATT	4366
864	3lnSerProSerLeuLeuAsnA	880
4367	ATCAAAAGCAAGGAGAAATGCAATGGTGGGAAATGGCACACGGTGGTGTT	4416
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897	rArgGluThrSerGluGluGlyHisPheArgLeuGlnLeuA	913
4461	CCCGGGAGGAAGTTTGCCTGGAAACTCCACCATCAGCATCA	4510
914		924
4511	TTACCTGGGATCACCTCCATCAGGGAAACCAAAGAGCCTCC	4560
925	.LysGlyPheLeuGlyCysIleArgSerLeuHisLeuAsnGlyGlnLysM	941
4561	AAACAGCTTTGTGGGATGCCTGAAGAACTTTCAGCTGGATTCAAAACCCT	4610
941	etAspLeuGluGluArgAlaLysValThrSerGlyValArgProGlyCys	957
4611		4657
958	ProGlyHisCysSerSerTyrGlySerIleCysHisAsnGlyGlyLySCy	974
7		- 20

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TTATGTGTTTACCTG 4828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4829 GAGGCA.....GGAAA 4839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4890 CACCAAAGCAGTCTCTGTGTGATGGACAGTGGCACTCGGTGGCAGTCACC 4939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1041 leAlaLeuSerPheValThrThrGlnAlaProSerLeuLeuLeuPheIle 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1058 AsnSerSerGlnAspPheValValValLeuLeuCysLysAsnGlySe 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1074 rLeuGlnValArgTyrHisLeuAsnLysGluGluThrHisValPheThrI 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4840 GGTCACGGCCTCTATGGACAGTGGGGCAGGTGGGACCTCAACGTCGGTCA 4889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1124 rTyrAsnPheSerProGluValGluPheArgValIleArgSerLeuThrL 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4990 AGCTGGACAGATCCCCTTCCCACCTGCCAGCACTCAAGAGCCACTACACC 5039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1141 euGlyLysValThrGluAsnLeu...GlyLeuAspSerGluValAlaLys 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5040 TTGGAGGTGCTCCAGCCAATTTGACGACACTGAGGATCCCTGTGTGGAAA 5089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1157 AlaAsnAlaMetGlyPheAlaGlyCysMetSerSerValGlnTyrAsnHi 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1173 sIle...AlaProLeuLysAlaAlaLeuArgHisAlaThrValAlaProV 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5128 CATCCCTGTCCCTGTCACTGAAGCCTTGGAA.....GTCCAGGGGCCTG 5171
                                                                                                                                     991 luGlyProPheCysLysLysGluValSerAlaValPheGluAlaGlyThr 1007
                                                                                                                                                                                                                                                                          1008 ServalThrTyrMetPheGlnGluProTyrProValThrLysAsnIleSe 1024
                                                                                                                                                                                                                                                                                                                                          .....ATCCGCCCAAGAAG 4767
                                                                                                                                                                                                                                                                                                                                                                                                            1024 rLeuSerSerAlaIleTyrThrAspSerAlaProSerLysGluAsnI 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4768 TCTCACTGGGATCCTAATACACATCGGAAGTCAGCCCGGGAAGCAC.... 4813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1091 leaspalaaspasnPhealaasnargargMetHisHisLeuLysIleAsn 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1108 ArgGluGlyArgGluLeuThrIleGlnMetAspGlnGlnLeuArgLeuSe 1124
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974 sValGluLysHisAsnGlyTyrLeuCysAspCysThrAsnSerProTyrG 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Tessler-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/191,647
CURRENT FILING DATE: 1998-11-13
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: 60/065,544
EARLIER APPLICATION NUMBER: 60/065,54
                                                                                                                                                                                                    4727 ..GGGCCA......GAATTTAAGCTTGTTTTCAGC......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/1/1na/6A_COMB.seq:US-09-191-647-1
                                                               4702 CGTCTTGGCTCACTCTGTTG.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5172 TCAGTCTGAATGGT 5185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1189 alThrValH1sGly 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4814
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1791 GTTCAAGGGATTGGAAAGCCTCAAAACTTTGATGTTGAGAAGCAATCGAA 1840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1991 GTAACTGCTACCTGGCTTGGTTGGGAGGTGGCTGAGAAGAAGAGAATT 2040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2041 GTCACGGG......AAATCCTAGATGTCAAAAACCATA 2072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2123 GTGATGACGGAAATGATGACAATAGTTGCTCCCCACTTTCTCGCTGTCCT 2172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2223 GAAGGICTIGCCGAAAGGIAITCCAAGAGAIGICACAGAGIIGIAICIGG 2272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1841 TAACCTGTGTGGGGAATGACAGTTTCATAGGACTCAGTTCTGTGCGTTTG 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1941 TACTCTCCATTCTTTATCTACTCTAAACCTCTTGGCCAATCCTTTTAACT 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ......IleThrPheValAsnSerSerGlySe 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 IleGluArgValGlyLysGlnValAsnPheThrValAspLysHisThr.. 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 ......GlnHisPheArgThrLysGlyGluThrAspA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 ...... 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....ProValProGlyLysProGlyThrPheLeuLysLys.....AsnP 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 heHisGlyCysIleGluAsnLeuTyrTyrAsnGlyValAsnIleIle*** 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .......GlyAsnValThrPheSerCysSerGluProGlnIleValPro 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 rTyrLeuLeuLeuProGlyThrProGln......IleA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spGlyLeuSerValSerPheGlnPheArgThrTrpAsnLysAspGlyLeu 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405 LeuLeuSerThrGluLeuSerGluGlySerGlyThrLeuLeuLeuSerLe 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uGluGlyGlyIleLeuArgLeuVal.....IleGlnLysMetT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 laLeuAspIle.....AspTyrGluLeuSerPheGlyGlyIle...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 875
Gaps: 50
Percent Identity: 21.943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-09-191-647-1 from: 1 to: 4758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 LeuAlaLysArgArgLysHis.GlnIleTyrThrVal...
EARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SCOTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 4758
TYPE: DNA
ORGANISM: human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-770-643A-2 x US-09-191-647-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2273 ATGGA.....AACCAATTT
                                                                                                                                                                                                                                                                                                                                                                  253.00
                                                                                                                                                                                                                                                                                                                                                                                                                    45.829
                                                                                                                                                                                                                                                                                                                                                                                               0.631
                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (1)..(4575)
US-09-191-647-1
                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313
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2440		2489
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521		7
7 7 7		2724
537 2725	eSerAspLeuHisIleAspLeuCysSerIleLysAspArgCysLeuProA   ::::::::	554 2761
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571	Cysasncys	573
574		. 985
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618 2968		635 3010
635		647
3011	AAAATAATTCTACATGTGTCGATGGCATTAATAACTACACATGC	3054
648 3055		661 3080
661	ა ე	676 3130

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9	AAGGGA	, <del>,</del>
70	TyrTrpGlyGlySerProProGlyValGlnGlnCysGluCysGly:	26
Ò	.Trcaarigisaciscacaccassgracsiassgraaca	~
726 3215	spGluSerCysLeuAspIleGlnH    :::::         ATTTGACGACTGCCAAGACAACAAGTGTAAAA	739 3264
740	Æ	750
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9	ATAATTTTGATTGTCAGAATGGAGCTCAGTGTATCGTCAGAATAAATGA	. 4
782	LeuArgCys	793 ·
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-	:    ::	9
828	1yProValGluLeuValValGlnSerProSerLeuLeuAsnAspAs	874
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2223 388	GAAGGTCTTGCCGAAAGGTATTCCAAGAGATGTCACAGAGTTGTATCT spG1yLeuSerValSerPheG1nPheArgThrTrpAsnLysAspG1yL
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448	
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2/25	snTyrCysGluH

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<₽	SerAspThrSerTyrThrGlyAlaThrCysHisAsnS	586
	GCATCAGTAACCCATGTAAACATGGAGGAACTTGCCAC	2907
586 erileTyrG	<pre>yrGluGlnSerCysGluValTyrArgHisGlnGlyAsnThrAla ;;;   ;;</pre>	602
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676 luGlnGluV :::::::	1uGluQalalaTyrHisCysArgArgSerArgLeuLeuAsnThrPro         11::::::                           AGCACGAT       TCAAAGTGCATCCTAACTCCA	692 3159
693 AspGlyThr	AspGlyThrProPheThrTrpTrpIleGlyArgSerAsnGluArgHisPr	709
3160 AAGGGA	 AAGGGA	3165
709 OTYRTREGI ::: 3166 TTCAAATG	oTyrTrpGlyGlySerProProGlyValGlnGlnCysGluCysGlyLeuA :::         TrcAaatgrGaCTGCACACGGTACGTAGGTGAACACTGCGACATGG	726
301		
	State	739 3264
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765 leThrAspT	leThrAspThrAspArgSerAsnSerGluAlaAlaTrpArgIleGlyPro	781
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808 heHisAlaG	heHisAlaGluPheSerAlaAspIleSerPhePheDheLysThrThrAla::::::::::::::::::::::::::::::::::::	824

	3565 G	December of year transfer of the control of the con	3611
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	858 ly 3659 Al		874 3705
	.: 3706 TI	TrpHisTyrValArgAlaGluArgAsnLeuLysGluThrSerLeuGlnVa E :::           ::	891 3755
•	891 17       3756 GC	laspasnLeuproArgSerThrargGluThrSerGluGluGlyHisp 9	907 3801
	907 he	heArgLeuGlnLeuAsnSerGlnLeuPheValGlyGly	919 3849
	920	ThrSerSerArgGlnysGlyPh 5 :::	927 3899
	927 eI   3900 CC	eLeuGlycysIleArgSerLeuHisLeuAsnGlyGlnLysMetAspLeuG 9	944 3948
	944 lu 3949	luGluArgAlaLysValThrSerGlyValArgProGlyCysProGly 5 ::::::::::::::::::::::::::::::::::::	959 3996
	960 Hi	HisCysSerSerTyrGlySerIleCysHisAsnGlyGlyLysCysValGl 9      :::    :::	976 4034
	976 uI :: 4035 CZ	rLeuCysaspCysThrasnSerProTyrGluGlyP :	993 4081
	993 rc     4082 CC	rophecysLysGluValser 1000   :::    ::::::::::  ccTrTgTGACCAACGGACCAAT 4104	
Š	eq_name: /	/cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-540-153-1	
<b>й</b>	99_documentat Sequence 1, Patent No. 6 GENERAL INFO APPLICANT: APPLICANT: APPLICANT: TITLE OF IN TITLE OF IN FILE REFERE CURRENT FILE PRIOR APPLI PRIOR APPLI PRIOR FILIN PRIOR FILIN PRIO	seq_documentation_block: Sequence 1, Application US/09540153 Patent No. 6270995 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Goodman, Corey APPLICANT: Goodman, Corey APPLICANT: Brose, Katja APPLICANT: Brose, Katja APPLICANT: Brose, Katja APPLICANT: Brose, Katja CURRENT APPLICATION NOMBER: US/09/540,153 CURRENT FILING DATE: 2000-03-31 PRIOR PILING DATE: 1998-11-13 PRIOR APPLICATION NUMBER: 60/081,057 PRIOR FILING DATE: 1998-04-07 NUMBER OF SEQ ID NOS: 14 SCO ID NO 1 LENGTH: 4758 TENGTH: 4758 CENTANTENT OF THE TENDER THE TENDER THE THE TENDER THE THE TENDER THE THE TENDER THE THE THE TENDER THE	

					300 1890	312 1940	312	1990	326 2040	342 2072	354 2122	368 . 2172	377 2222	388 2272	404 2289	421 2339	434 2389	447 2439	460
FEATURE: NAME/KEV: CDS LOCATION: (1) . (4575) S-09-540-153-1	alignment_scores: Quality: 253.00 Length: 875 Ratio: 0.631 Gaps: 50 Percent Similarity: 45.829 Percent Identity: 21.943	alignment_block: US-09-770-643A-2 x US-09-540-153-1	Align seg 1/1 to: US-09-540-153-1 from: 1 to: 4758	274 IleGluargValGlyLysGlnValAsnPheThrValAspLysH1sThr 2 ::::: :::	290GlnHisPheargThrLysGlyGluThrAspA 3	300 laLeuAspIleAspTyrGluLeuSerPheGLyGlyIle 3	312 3	CCTTTTAACT	313ProValProGlyLysProGlyThrPheLeuLysLysAsnP 3	326 heHisGlyCyslleGluAsnLeuTyrTyrAsnGlyValAsnIleile*** 3                   GTCACGGGAATCCTAGATGTCAAAAACCATA 2	343 LeualaLysargargLysHis GinileTyrThrVal	355GlyAsnValThrPheSerCysSerGluProGlnIleValPro 3	369IleThrPheValAsnSerSerGlySe 3 ::::: ::::!   :::::::!   :::::::    :::::::    ::::::::	377 rTyrLeuLeuLeuProGlyThrProGln	388 spGlyLeuSerValSerPheGlnPheArgThrTrpAsnLysAspGlyLeu 4	405 LeuLeuSerThrGluLeuSerGluGlySerGlyThrLeuLeuSerLe 4	421 uGluGlyGlylleLeuArgLeuVallleGlnLysMetT 4	434 hrGluargValalaGluIleLeuThrGlySerAsnLeuAsn 4 [ ::::::::   ::::::   ::::::   ::::::   ::::	448AspGlyLeuTrpH1sSerValSerIleAsnAlaArgAr 4

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. 2968	ACTGT	3010
635	- S	647
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676	LuValAlaTyrHisCysArgArgSerArgLeuLeuA :: ATTCAAAGTGCATCC	692 3159
693	AspGlyThrProPheThrTrpTrpIleGlyArgSerAsnGluArgHisPr	709
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976 uLysHisAsnGlyTyrLeuCysAspCysThrAsnSerProTyrGluGlyP 993
                                                                                                                                               seg_name: /cgn2_6/ptodata/1/ina/5A_COMB.seg:US-08-644-271-31
                                                                                                                                                                                                 Sequence 31, Application US/08644271
Patent No. 5814478
GENERAL INFORMATION:
APPLICAMY:
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS
TITLE OF INVENTION: AND LIGANDS
NUMBER OF SOURNINGS: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Regeneron Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 496
Gaps: 25
Percent Identity: 24.395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 1479
                                                                                                                                                                                                                                                                                                                                                        E: Regeneron Pharmaceuticals, Inc. 777 Old Saw Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/644,271
FILING DATE: 10-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: 15-DEC-1995
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REG 195A
                                                                                           4082 CCCTCTGTGACCAACGGACCAAT 4104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                        993 roPheCysLysLysGluValSer 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-644-271-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-770-643A-2 x US-08-644-271-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36,108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Coding Sequence LOCATION: 1...1476
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1479 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Cobert, Robert J
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Human Agrin LOCATION: 1...1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235.50
0.916
51.815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION US-08-644-271-31
                                                                                                                                                                                      seg_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                         Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10591
                                                                                                                                                                                                                                                                                                                                                                                                                ΝŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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715	ProProGlyValGlnGlnCysGluCysGlyLeuAspGluSerCysLeuAs	731
124	CCCAAGGGTGCTCAGTGCGAGTGCCCCTGGGGCGTGAG	165
731	IlecinhisPhecysAsnCysAspAlaAspLysAspGluTrpThrAsn	₹ (
748	### apthrGlyPheLeuSerPheLysAspH1sLeuProValThrGlnIleVal	198
1.98		σ
765	pArgSerAsnSerGluAlaAl	781
199		209
781 210	oLeuArgCysTyrGlyAspArgArgPheTrpAsnA  ::: CTTC	798 226
798	rTyr	
122	ACCOUNTINGE CANCEL CARGO CONTRACTOR CANCER C	_ (
	ASP	825 323
825 324	uSerGlyValPheLeuGluAsnLeuGlyIleLysAspP        :::::   	838 373
838 374	helleArgLeuGluIleSerSerProSerGluIleThrPheAlaIleAsp 	854 420
855 421	ValGlyAsnGlyProValGluLeuValValGlnSerProSerLeuLeuAs :::    :::	871 464
871	nAspasnGlnTrpHisTyrValArgAlaGluArgAsnLeuLysGluThrS::::::::::::::::::::::::::::::::::::	888
465	CTGGGAGCCTGGACCAGGGTCTCACTGGAGCGAAACGCCGCAAGGGTG	514
888 515	erLeuGlnValAspAsnLeuProArgSerThrArgGluThrSerGluGlu::   :::   :::::::::::::::::::::::	904 564
905 565	CGCAAGGTTCCGCACACACCTCAACGAGAGAGCCGCTCTACGAGGAGCCGCTCTACGAGGAGCCGTCTAACGTAGGAGCCGCTCTAACGTAGG	918 614
918	yGlyThrSerSerArgGlnLy8	926
615	GGGCGCTCCCGACTTCAGCAAGCTGGCCCGTGCTGCTGCCGTGTCCTCTG	664
926 665	lyPheLeuGlyCysIleArgSerLeuHisLeuAsnGlyGlnLySMetAsp 	942 714
943	LeuGluGluArgAlaLysValThrSerGlyValArgPr                                  ACCCGGAGCACGTGCAGGTGGAGGTCACGTCA	955 753
955	CysHis	026
754		662
970	snGlyGlyLysCysValGluLysHisAsnGlyTyrLeuCysAspCysThr 	80 4
987		1000

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1061 erGln.....AspPheValValLeuLeuCysLysAsnGlySerLeu 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1092 palaaspasnPhealaasnArgargMetHisHisLeuLysIleasnArgG 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1176 GCCCGTCAAC. ... ACCAACCGCTGGTTGCGGGTCGTGGCACATAGGG 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1126 AsnPheSerPro.....GluValGluPheArgValIleArgSerLeuTh 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1267 GCTCCTCCCCCGCTGGGCGCCACGCAGCTGGACCATGATGGAGCCCTGTG 1316
                                                                                                                                                                                                                                                                                                                              1076 GlnValArgTyrHisLeuAsnLysGluGluThrHisValPheThrIleAs 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1126 CAACTGAGCTACAACCTGGGCTCCCAGCCGGTGGTGCTGCGTTCCACCGT 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1109 luGlyArgGluLeuThrIleGlnMetAspGlnGlnLeuArgLeuSerTyr 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1140 rLeuGlyLysValThrGluAsnLeuGlyLeuAspSerGluValAlaLysA 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....ValPheGluAlaGlyThrSerValThrT 1011
                                                                                                                                                                                     1011 yrMetPheGlnGluProTyrProValThrLysAsnIleSerLeuSerSer 1027
                                                                                                                                                                                                                                                                                               1028 SerAlaIleTyrThrAspSerAlaProSerLysGluAsnIleAlaLeuSe 1044
                                                                                                                                                                                                                                                                                                                                                                                                       1044 rPheValThrThrGlnAlaProSerLeuLeuLeuPheIleAsnSerSerS 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onlyst, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT PILLICATION NUMBER: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SEQ ID NO 64
LENGTH: 2481
                                                                                                               850 GGGGGA...TTCTCAGGACCGCACTGCGAGAAGGGGCTGGTGGAGAAGTC 896
                                                                                                                                                                                                                                             947 ACCTC.....AACGCTGTGACCGAG.....AGCGAACTGGCC 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-09-188-930-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1157 laAsnAlaMetGlyPheAlaGlyCysMetSerVal 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1364 CCTACGGCACAGGCTTTGTGGGCTGCTTGCGGGACGTG 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
; Sequence 64, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
                                                                           1000 rAla....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Rat
US-09-188-930-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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alignment\_scores:

lignment_bl US-09-770-6	Align seg 1/1 to: US-09-188-930-64 from: 1 to: 2481	335 TyrAsnGlyValAsnIleIle***LeuAlaLysArgArgLysHisGlnII 351    :::::::::::       :::        55 TACAAACATTTAACACTTATAGACTTAAGTAACAACAGAAT 95	351 eTyrThrValGlyAsnValThrPheSerCysSerGluProGlnIleValP 368       ::::::    :::          :::        :::::::	8 rolleThrPheValAsnSerSerGlySerTyrLeuLeuLeuProGlyThr 38	ProGlnIleAspGlyLeuSerValSerPheGlnPheArgThrTrpAsnLy 40	LeuSerThrGluLeuSerGluGlySerGlyThrLe	luGlyGlyIleLeuArgLeuValI ::   ::: ATGGAATGACATTTCTGTCGTGC	434ThrGluargValalaGluIleLeuThrGlySerAsn 445 :::::::::::::::::::::::::::::	446LeuAsnAspGlyLeuTrpHisSerValS 455	ThrLeuAspAspGlu      GAATTG	er.G	488SerTyrTyrPheGly.GlyCysProAspAsnLeuThrAspSerG 502 :::::    ::::	502 lnCysLeuAsnProlleLysalaPheGlnGlyCysMet 514 ::	515 ArgLeullePheileAspAsnGlnProLysAspLeuIleSerVa 529 :::	529 lGlnGlnGlySerLeuGlyAsnPheSerAspLeuHisTleAspLeuCysS 546	546 erilelysAspArgCysLeuProAsnTyrCysGluHisGlyGlySerCys 562 ::	563SerGlnSerTrpThrThrPheTyrCysAsnCysSe 574 :::::     ::::    :: 646 CATTTAAAACCAAGGAGAGAACATGGATTTGGTGTACTTGTGC 689
Ø																	

591	erCysGluValTyrArgHisGlnGlyAsnThrAlaGlyPhePheTyrIle	607
3		m
608	SerAspGlySerGlyProLeuGlyProLeuGlnValTyrCysAsnI	624
739	GATAATGATTGT	750
624	eThrGluAspLysIleTrpThrSerValGlnHisAsnAsnThrGluLeuT	641
751	GAAAATAATTCTA	763
641	hrArgValArgGlyAlaAsnProGluLys	650
764	CATGCGTTGATGGAATTAACAACTACACGTGTCTTTGCCCACCGGAA	810
651	<pre>!yrAlaMetAlaLeuAspTyrGlyGlySerMet</pre>	999
811	THE	839
665	uGluAlaValIleAspGlySerGluHisCysGluGlnGluValAlaTyrH	682
840	GGACTICTGTGCACAAGACCTGAATCCCTGCCAGCATGAC	879
682	isCysArgSerArgLeuLeuAsnThrProAspGly	694
880	TCCAAGTGCATCCTGACGCCAAAGGGATTCAAGTGTGAC	918
695	ThrProPheThrTrpTrpIleGlyArgSerAsnGluArgHisProTy	710
919	TGCACTCCGGGATACATTGGT	939
710	rTrpGlyGlySerProProGlyValGlnGlnCysGluCysGlyLeuAspG	727
940	GAGCACTGTGACATTGATG	964
727		743
965	ACTGCCAAGATAACAAGTGCAAAAACGGTGCTCATTGCACA	1005
744	luTrpThrAsn.AspThr	749
1006		1055
750		759
1056		$\ddot{-}$
160	nrGlnIleValIleThrAspThrAspArgSerAsnSerGlu	774
1103		1149
775		782
1150		1189
782	rgCysTyrGlyAspArgArgPheTrpAsnAlaValSerPheTyrT	798
1190	STGTGAGAAATTGGTCAGTGTCAATTTTGGTAA	1228
798	AlaSerTyrLeuHisPheProThrPheHisAlaGluPheSerAla	-
1229	<u> AAAGAGTCCTATCTTCAGTTCCTTCAGCCAAGGTTCGACCTCAGACA</u>	7
815	PheLysThrThrAlaLeuSerGlyValPheLeuGl :::	831
7	CAICACACIICAGAIIGCCACAGAIGAAGACAGCGGCAICCICIIGIA	7 7
831	G	848

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APPLICANT: Rawal, Shinji
APPLICANT: Takeshita, Sunao
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Carboxypeptidase-Like
TITLE OF INVENTION: Protein and Process for its Production
NUMBER OF SEQUENCES: 27
CORRESPONDENCES: 27
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
1370 GCATTCGAGCCAGCTATGACACCGGCTCTCACCGGCTTCT...GCCATT 1416
                                                                                                                                                                                                                                                                          1467 GACCCTGGATTCGAGTCTTTCCCTCTCTGTGGATGGAGGAAGCCCTAAAA 1516
                                                                                                                                                                                                                                                                                                                                                                     1517 TCATCACCAATTTGTCAAAACAATCT.....ACTCTGAATTTGGACTT 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1611 CCAGGCCCCTGGGCAGAACGGCACCAGCTTCCATGGCTGTATCCGGAACC 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          983 ysAspCysThrAsnSerProTyrGluGlyProPheCysLysLysGluVal 999
                                                                                                                                                          865 GlnSerProSerLeuLeuAsnAspAsnGlnTrpHisTyrValArgAlaGl 881
                                                                                                                                                                                                                                                   881 uArgAsnLeuLysGluThrSerLeuGlnValAsp...AsnLeuProArgS 897
                                                                                                                                                                                                                                                                                                                                            897 erThrArgGluThrSerGluGluGlyHisPheArgLeuGlnLeuAsnSer 913
                                                                                                                                                                                                                                                                                                                                                                                                                                  914 GlnLeuPheValGlyGly.....ThrSerSerAr 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         923 gGln......LysGlyPheLeuGlyCysIleArgSerL 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    euHisLeuAsnGlyGlnLysMetAspLeuGluGluArgAlaLysValThr 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     966 rIleCysHisAsnGlyGlyLysCysValGluLysHisAsnGlyTyrLeuC 983
                                                                   848 lulleThrPheAlaIleAspValGlyAsnGlyProValGluLeuValVal 864
                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/1na/5A_COMB.seq:US-08-111-939-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPBAIDLE
OPPERATING SYTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington
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:::|||||| :::::|||:::
1287 CGCCTCAACATGCAGGCTGCCAATGAAGATGACTACTATGACGGGGC 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....SerAspTrpValThrSerTyrSerLeuMetPheSerAspThrGl 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 yArgAsnTrpLysGlnTyrLysGlnGluAspSerIleTrpThrPheAlaG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 lyAsnMetAsnAlaAspSerValValHisHisLysLeuLeuHisSerVal 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 ArgAlaArgPheValArgPheValProLeuGluTrpAsnProSerGlyLy 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 yTrpSerProAlaAspSerAsnAlaGlnGlnTrpLeuGlnMetAspLeuG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 lyAsnArgValGluIleThrAlaValAlaThrGlnGlyArgTyrGlySer 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 GlnLeuAsnTrpArgValGlyThr.....GlyGl 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 771
Gaps: 39
Percent Identity: 20.493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 3728
                                                                                                                                                                                                                NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 02481.1321-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: osteoblastic cell line MC3T3E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUBER: JP 324033/92
FILING DATE: 03-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUBER: JP 230029/92
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
                  UMBER: US/08/111,939
26-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-111-939-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-770-643A-2 x US-08-111-939-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 26-AUG-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222.00
0.645
44.617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
US-08-111-939-1
                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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1631	CCTGTGCATGCGCCTGGAGGTGCTAGGCTGCCCCGTGACCCCTGTCTACA	1680
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201		203
1772	CAATGAGGAGTGCCCCACAAT	1821
204	vallleSerLeuLysPheLysSerMetGlnGlyAsp	215 1871
216 1872	GlyvalLeuPheHisGlyGl     :::      :: CATGAACTGGGGGAGCCCGAGTTCCGCTACACAGGCGGGATCCACGGCAA	222 1921
222		239 1968
239		255 2003
256 2004		272 2035
272		289
2036		2036
289	hrG	304
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315 2106	oGlyLysProGlyThrPheLeuLysLysAsnPheHisGlyCysIleGluA	332 2139
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649	ValArgGlyAlaAsnProGlu	543
	. AGGGCGTCTACAGTACCGGCTCCGCATGAGGGAACAGATGCAACT	. 0
, ,	necessaria de la composición de la composición de la company de la compa	3 6
626 3099	Thr	610 3058
610 3057	uValTyrArgHisGlnGlyAsnThrAlaGlyPhePheTyrIleAspSerA  :::   :::               GATCTTGGCTATGAACGGGAACCGTCCCATTCTCGGAGTTG	593 3017
593 3016	ThrCysHisAsnSerIleTyrGluGlnSer	582 2967
581 2966	erirpinrinrPneTyrCysAsncysSerAspInrSerIyrInrGiyAla :::::   :::  CTACACCTCAAGIGCCAAGATCTGCAATGIGGACTACGATATTGGGGCC	565 2917
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528 2716	GlyCysMetArgLeuIlePheIleAspAsnGlnProLysAspl           GGTGTGACAAGTTCCCCCACGAGAGTGAGCTACCCCGAGAAI	512 2667
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499	:	495
494 2569	ACGGAGCCCTACCAGGCCCAGGACTACACCAGGCCAT	490
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4	GAT	CI.
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682 H1sCysarg 684            3260 CACTGCAGG 3268	
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seq_documentation_block:     Sequence 1, Application US/08706216     Patent No. 6140098     GENERAL INFORMATION:     APPLICANT: Balasubremmanian, Sriram	
### APPLICANT: FORG, JOHN ### APPLICANT: Gorman, Daniel M. ### APPLICANT: Zurawski, Gerard #### TITLE OF INVENTION: MAMMALIAN PROTEASES; RELATED REAGENTS #### NUMBER OF SEQUENCES: 6	
CORRESPONDENCE ADDRESS: ADDRESSEE: DNAX Research Institute STREET: 901 California Avenue CITX: Palo Alto	
STATE: California COUNTRY: USA ZIP: 94304-1104	
COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible	
) OPERATING SYSTEM: PC-DOS/MS-DOS SPENDENT PALENTIN Release #1.0, Version #1.30 CHORENT APPLICATION DATA:	
APPLICATION NUMBER: US/08/706,216 FILING DATE: 30-AUG-1996	
ATTORNET LAND.  ATTORNET Ching, Edwin P.	
REGISTRATION NUMBER: 34,090 REFERENCE/DOCKET NUMBER: DX0613 TELECOMMUNICATION INFORMATION:	
: TELEFHONE: 415-496-1200 : TELEFAX: 415-496-1200 : INFORMATION FOR SEO ID NO: 1:	
ω±	
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210	LysSerMetGlnGlyAspGlyValLeuPheHisGlyGluGlyGlnAr 2	364
225 1365	2 4	374
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292	. 3	524
309	<u>ო</u> -	125

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seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-746-111	4
q_documentation_block: Sequence 4, Application US/08746111 Patent No. 6066788 GENERAL INFORMATION: APPLICANT: Ginsburg, David APPLICANT: Ginsburg, David APPLICANT: Ginsburg, David APPLICANT: Cui, Jisong TITLE OF INVENTION: Compositions And Methods For Andrews STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco CITY: San Francisco STATE: California COUNTRY: United States of America 2 IP: 94104 COMPUTER: EBADABLE FORM: MEDTUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PAtentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/746,111 RECIEGATION NUMBER: UM-02536 TELEPONE: (415) 397-8138 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 6558 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA" FEATURE: NAME: VESS COS COS CONDORNESS: NAME/KEY: CDS LOCATION: 6.6554	Screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 ArgPheValArgPheValProLeuGluTrpAsnProSerGlyLyslleGl 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 lulleThrAlaValAlaThrGlnGly.....ArgTyrGlySerSerAsp 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 sGlnTyrLysGlnGluAspSerIle.....TrpThrPheAlaGlyAsnM 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-936-135-11
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6177 TCCCTTGCCGGCTGAACGCCCAAGCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                           54 SerProAlaGlnLeuAsnTrpArgValGlyThrGlyGlyTrpSerProAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 TrpValThrSerTyrSerLeuMetPheSerAspThrGlyArgAsnTrpLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 aAspSerAsnAlaGlnGlnTrpLeuGlnMetAspLeuGlyAsnArgValG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE PATENTIN STATES SOFTWARE SOFTW
     Gaps: 36.800
                                                                                                                                                                                                                                                                                                        to: 6585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
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    Patent No. 6054293
    GENERAL INFORMATION:
    APPLICANT: Tessier-Lavigne, Marc APPLICANT: He, Zhigang
    APPLICANT: He, Zhigang
    APPLICANT: Glan, Hann
    TITLE OF INVENTION: Semaphorin Receptors
    NUMBER OF SEQUENCES: 26
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 sSerValArgAlaArgPheValArgPheValProLeuGluTrpAsnProS 162
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TOPOLOGY: linear
NOLECULE TYPE: CDNA
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(650) 343-4342
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0.622
43.258
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245 2649	CGAGAGGCCAGTACGGCGCGCTCATCACCCGCTGCCCCG	250 2698
251 <sup>°</sup> 2699	AGCCCTGTGTGCATGGAGTTCCAGTACCAGCCATGGGCGGCCACGGG	261 2748
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3297	420 3347	430 3397	438 3447	454 3470	471 3514	488 3533	504 3551	521 3583	538 3616	554 3643	561 3693	578 3743			ECIFITY AND CLOTTING OLOGIES, AND POLYRIBO-IDE, ANTI-METHODS OF
3254 CGATGGCCTCAAGCACAAGGTCAAGATCATCAGAAGTGCT	411SerGluGlySerGlyThrLeuLeuLeuSer	421 LeuGluGlyGly1leLeuArgLeuVallIe	431	438 laGluIleLeuThrGlySerAsnLeuAsnAspGlyLeuTrpHisSerVal :::::	455 SerIleAsnalaArgArgAsnargIleThrLeuThrLeuAspAspGluAl :::		488 erTyrTyrPheGlyGlyCysProAspAsnLeuThrAspSerGlnCysLeu    :::    3534TGGCCAAGTGAATGCAGG	505 AsnProlleLysAlaPheGlnGlyCysMetArgLeullePhelleAspAs	521 nGlnProLysAspLeulleSerValGlnGlnGlySerLeuGlyAsnPheS	538 erAspLeuHisIleAspLeuCysSerIleLysAspArgCysLeuProAsn	555 TyrcysGluHisGlyGlySe :::   :::	561 rcysSerGlnSerTrpThrThrPheTyrCysAsnCysSerAspThrSerT	578 yrThrGlyAlaThrCysHisAsnSerIleTyrGluGInSerCys 592 ::	seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-07-607-538C-1	seq_documentation_block:     Sequence 1, Application US/07607538C     Patent No. 545501     Patent No. 545501     APPLICANT: Ceriani Dr., Roberto L.     APPLICANT: Ceriani Dr., Jarry A.     APPLICANT: Larocca, David J.     TITLE OF INVENTION: POLYPEPTIDE WITH 46     TITLE OF INVENTION: POLYPEPTIDE WITH 46     TITLE OF INVENTION: FUSION PROTEIN, POLYNUCLEOTIDE AND POLY TITLE OF INVENTION: PUSION PROTEIN, POLYNUCLEOTIDE AND POLY TITLE OF INVENTION: POLYPEPTIDE BROCODING THE POLYPEPTIDE, ANT TITLE OF INVENTION: POLYPEPTIDE ANTIBODIES, KITS AND METHODS; TITLE OF INVENTION: USE THEREOF     TITLE OF INVENTION: USE THEREOF     CORRESPONDENCE ADDRESS:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 CAGGCCTCCAGCAGCTACAAGACCTGGGGCTTGCATCTCTTCAGCTGGA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 ACCCTCCTATGCACGCTGGACAACAGCAACTTCAACGCCTGGGTT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 erAspTrpValThrSerTyrSerLeuMetPheSerAspThrGlyArgAsn 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431 TCCAGTTTGTGGCATCCTACAAGGTTGCCTACAGTAATGACAGTGGCGAAC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 TrpLysGlnTyrLys.....GlnGluAspSerIleTrpThrPheAlaGl 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 .....SerProAlaGlnLeuAsnTrpArgValGlyThrGlyGlyTrpSer 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 CysAspAspProLeuAla.....SerLeuLeuSerProMetAl 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 aPheSerSerSerAspLeuThr...GlyThrHis......
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/607,538C
FILING DATE: 01-NOV-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: V1viana Amzel
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRFCC-004
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELEFAX: (510) 943-1189
TELETE NA.
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1384 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 11
Percent Identity: 29.870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-07-607-538C-1 from: 1 to: 1384
ADDRESSEE: V. Amzel & Assoc.
STREET: 2055 No. 5455031th Broadway
CITY: Walnut Creek
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-770-643A-2 x US-07-607-538C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:

Quality: 200.00
Quality: 1.481
Percent Similarity: 58.442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear ; MOLECULE TYPE: CDNA US-07-607-538C-1
                                                                                                    USA
                                                                                                 COUNTRY:
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	786 CACAGTCACCCTCCCTCTTTCCCACCCTCCACCTCTA 828	786
	GluLeuGlnLysGlyArgLe	22
785	-	754
229	lyAs	21:
753	## CCTCTTGGCTTCTCAGCCCCTTTAAATCACCATAGGGCTGGGGACTGGG 753	704
212	LeuLysAspVal	19(
703	669 CACCCCCAGGTCTTCCTGCTTTCCATGGGCCGGCT 703	99
196	179 pvalAlaAspPheAspGlyArgSerSerLeuLeuTyrArgPheAsnGlnL 196	17
668		619
179	163 GlyLysileGlyMetArgValGluValTyrGlyCysSerTyrLysSerAs 179	16
618	575 CCATCCTGGCTCTGTATGTGCGCATCCTGCCTGTAGCCTGGCAC 618	575
162	147ValArgAlaArgPheValArgPheValProLeuGluTrpAsnProSer 162	14
574	531 CAACTGGGACAACCACTCCCACAAGAAGAACTTGTTTGAGACGC 574	53